BH613513 SALK_0343 BH214265 SALK_0104 T60367 y90h09.r1 A432574 A472554 BE730257 601563625 BC739877 BC73625 BC739877 BC73625 BC7388196 TETERAGON BC738835 AGENCOURT BM47253 AGENCOURT BM572831 AGENCOURT AL341794 TETRAGON BM603553 1031111C0 BM57681 SALK_0145 AM561182 UI-HF-BP0 BT233181 CH-BP0 BT233181 CH-BP0

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ABC13513 BH214265 T60367 AJ478560 AJ432574

CC011462 AA803400 AA538677

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802 bp DNA linear GSS 17-DEC-2002 msh2_1835.x1 msh Pseudomonas aeruginosa genomic clone msh2_1835, genomic survey sequence.
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Spencer, D. H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol., (2002) In
Contact: Chris K. Raymond
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Pseudomonas aeruginosa
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                                                                                          August 27, 2003, 18:01:39; search time 2272.12 Seconds (without alignments) 363.693 Million cell updates/sec
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                                                                                                                                                                                                                                                                     45562784
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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34
1 cgattetttgetaetggetgeagetgeageeeg 34
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                                                                                                                                                                                                                                         22781392 seqs, 12152238056 residues
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Maximum Match 110%
Listing first 45 summaries
                                                                   OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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BG424809 G02455459 BG33558 G0240381 BL652558 G0240581 BL10369 G03067939 BL14059 G03067939 BG717956 G02698932 BG717465 G02698932 BG717465 G02698932

BF431634 7016f11.x B1866970 ft67a07.x CD358712 AGENCOURT AL296288 Tetraodon BU193557 AGENCOURT

ALIGNMENTS

Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, USA Tel: 20620216954 Fax: 2066857244 Email: craymond@u.washington.edu

Location/Qualifiers

Class: shotgun.

FEATURES

BZ571326 msh2_1835 AL211728 Tetraodon BM037193 fu84c01.y AA739600 365 PtIFG

BZ571326 CNS02SD3 BM037193 AA739600

802 910 438 660

71.8 68.8 67.6 67.6

24.4 23.4 23

H 22 E 4

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Description

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Query Match Length

Score

Result . 9

BU500183 AGENCOURT

BI545634 BG717956 BF984839 BG717465 BU594473 BU500183

BI562582 BG911254 BI910096

0;

Gaps

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EST 05-NOV-2001

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/dev_stage="4-5 month"
//dab_host="DH10B (phage-resistant)"
/clone_lib="Gong zebrafish ovary"
/clone_lib="Gong zebrafish ovary"
/note="Organ: ovary (pooled); Vector: pBluescript SK-;
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
the ovaries of 2 female adult zebrafish (4-5 month old).
cDNAs were made using oligo-dr primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. 2. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
University protocol
                                                                                                                                                                                                                                                                                                                                                      fu84c01.y1 Gong zebrafish ovary Danio rerio cDNA clone
IMAGE:5377536 5' similar to SW:PWM2_HUMAN 015305 PHOSPHOMANNOMUTASE
2; mRNA sequence.
BM037193. GI:16750764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l (bases 1 to 438)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ZDrafish@watson.wustl.edu
The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
High quality sequence stop: 323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Wilson,R.

Wash Zebrafish EST Project 1998
Unpublished
Contact: Stephen L. Johnson
Washington University School of Medicine
W444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                   Length 910;
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  6 others
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                                            Score 23.4; DB 29; I
Pred. No. 3.7e+02;
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  243 t
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/db_xref="taxon:7955"
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  221
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Danio rerio
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81.8%;
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                                                                                                                       27; Conservative
  192
                                                                   Query Match
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  248 a
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Direct Submission

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-nd sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS02SD3 910 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 161J22 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Flizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                           /clone_lib="msh" //clone_libarironmental isolate. Whole genomic shotgun
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PUC-Ori"
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0
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Pred. No. 1.6e+02;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                  348 CGATGCTTTGCTAGCGGCCGCATCTGCAGCGCCG 315
                                                                                                                                                                                                                                                                                                                                                                                      1 CGATICITIGCTACTGGCTGCAGCTGCAGCCCCG 34
                                                                                                                                                                                                                     228 t
                                                 /mol_type="genomic DNA"
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                                                                                                                                                                                                                   164 g
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Tetraodon nigroviridis
                                                                                                                         /clone="msh2_1835"
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a B

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Location/Qualifiers

1. 704

1. 704

/organism="zea mays"
/mol_type="ganomic DNA"
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/clone="zwkBra185E14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 23-APR-2001
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 704)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="newly eclosed females: germarium-stage 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA803400 603 bp mRNA linear EST 23-API GM10776.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM10776 5prime similar to X78555: CalpA FBgn0012051 PID:9562289 SMISS-PROT:011002, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Roptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lawrence Berkeley National Lab
Conforton Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 107 zow: G column: 4
High quality sequence stop: 488.
Location/Qualifiers
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Pred. No. 6.7e+02;
0; Mismatches 4; Indels 0:
                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .603
/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
/clone="GM10776"
                                                                                                                                                                                                                                                                   Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                Unpublished
Contact: Cathy Whitelaw
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AA803400.1 GI:2872519
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86.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="female
                                                                                                                                                                                                                                                                                                                 Seq primer: TF
Class: sheared ends
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Matches 25; Conservative
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/clone_lib="PtIFG2"
/note="vector: lambda ZaP; Site_1: EcoRI; Site_2: XhoI;
/note="vector: lambda ZaP; Site_1: EcoRI; Site_2: XhoI;
The tissue source for this library is xylem. The xylem
tissue was harvested in spring and summer from branches
of seed orchard trees which are clones of the same
genotype. Branches were 4.6 inches in diameter. The cDNAs
were directionally cloned into Lambda Zap and were
rescued as a Bluescript derivative in the EcoRI and XhoI
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: csk6s27w007.pswfs.gov
The sequence entry for this EST has been reverse complimented and
is being submitted in the sense orientation.
Seq primer: M13_Universal.
Location/Qualifiers
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USDA IRG Dendrome Project
Institute of Forest Genetics
Bendrome Project, Institute of Forest Genetics, P.O. Box 245,
Berkely, CA 94701
Tel: 5105596429
                                         Gaps
                                                                                                                                                                                                                                                  AA739600 660 bp mRNA linear EST 15
365 PtIFG2 Pinus taeda cDNA clone 8604M 3', mRNA sequence.
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              83.9%; Pred. No. 4.3e+02;
tive 0; Mismatches 5;
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Best Local Similarity 83.9%; Pred. No. 4.8e+02;
Matches 26; Conservative 0; Mismatches 5;
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                                                                                                           379 CGATTCTTTCCTGTTGCCTGCAGCTTCGGCC 349
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                                                                                   1 CGAITCITTGCIACTGGCIGCAGCTGCAGCC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pinus taeda"
/mol_type="mRNA"
/db_xref="taxon:3352"
/clone="8604M"
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                                                                                                                                                                                                                                                                                                                                                                  Pinus taeda (loblolly pine)
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Unpublished
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              Best Local Similarity 83.9
Matches 26; Conservative
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CC011462.1
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 180)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
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                                                                                                            SAIK_034371 Arabidopsis thaliana TDNA linear GSS 04-JAN-200 thaliana genomic clone SAIK_034371, genomic survey sequence. BHG13513.1 GI:18062637 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="SALK_334371"
/clone="SALK_334371"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/clone_lib="Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html
45 c 38 9 55 t
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A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of Atig20480.
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Salk Institute Genemic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 855 453 4100 x1752
Fax: 855 858 6379
Email: ecker@salk.edu
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7.9e+02;
5;
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/mol_type="genomic DNA"
/strain="Columbia 0"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                       545 CGATTGCTGCTACTGGCTGCACTGC 571
27
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1 CGATICITIGCIACIGGCIGCAGCIGC
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L Similarity 83.3%;
25; Conservative (
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Unpublished
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                /clone_lib="GM Drosophila melanogaster ovary BlueScript"
//orone_logan: ovary; Vector: BlueScript SK; Site_l: EcoRI;
Site_l: XhoI; Constructed using Stratagene ZAP-CDNA
Synthesis kit. Ollgo dT-primed and directionally cloned at
EcoRI and XhoI in BlueScript SK(+/-)"
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LD18261.5prime LD Drosophila melanogaster embryo Bluescaript
Drosophila melanogaster cDNA clone LD18261 5 similar to CalpB:
FBan008107 'Calpain' located on: 31 6703-6703;: 04/10/2001, mRNA
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BDGP/HHMI Drosophila EST Project
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003550: arm:31 [9682134,9979619]
estimated-cyto:67C1-67C9: 04/10/2001
Plate: LD.182 row: F column: 1
                                                                                                                                                                                                                                                        Gaps
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/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
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                                                                                                                                                                                                    Score 22.2; DB 9; Length 603; Pred. No. 8.9e+02; 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="BDGP_BST:BDcln017400"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                        262 CGATTGCTGGCTACTGGCTGCAGCTGC 288
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1..611
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  /lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.3%;
88.9%;
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88.9%;
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                                                                                                                                                                                                                                                      24; Conservative
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                                                                                                                                                                                                                                 Local Similarity
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AA538677
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Hordeum vulgare
Bukaryochyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum
1 (bases 1 to 480)
Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
Barley EST's
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                         dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZaP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Stratagene liver"(#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site_l: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ478560 800011 Hordeum vulgare cDNA clone 80001100114604F1, mRNA
                                        Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
High quality sequence stop: 209.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute of Biotechnology
University of Helsinki
P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 1.2e+03;
0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                /lab_host="SOLR cells (kanamycin resistant)"
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/clone_llb="800011"
/note="12,15,18 days after pollination"
in 171 c 137 g 78 t
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/organism="Hordeum vulgare"
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/db_xref="taxon:4513"
/clone="S0001100114G04F1"
                                                                                                                                                                                                                                                                                                                     /dev_stage="49 years old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CICGAGITITITITITITITITITIT
                                                                                                                                                                                 1. .320
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 TGCTACTGGCTGCANCTCCAGCCCTG 72
Email: est@watson.wustl.edu
High qality sequence stops: 209
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                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="GDB:498242"
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/clone="IMAGE:78497"
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AJ478560.1 GI:21194515
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78.8%;
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ilarity 88.5%;
Conservative (
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Matches 26; Conserv
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AJ478560
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubque, T., Favello, A., Galsh, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E.,
Underwook, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280, 000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160367 320 bp mRNA linear EST 13-FEB-1995 yb90h09.rl Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78497 5' similar to gb:J04449 CYIOCHROME P450 IIIA4 (HUMAN);
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                                           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="SAIK_010491"
/clone="SAIK_010491"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

48 c 47 g 58 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                             This is single pass sequence recovered from the left border of TDNA. This sequence lies within an intron of At1g20480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                   ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Limmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
(bases 1 to 196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 28; Length 196;
Pred. No. 8e+02;
                                                                                                                                                                       Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .196
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.7%;
83.3%;
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r60367.1 GI:663404
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                                                                                                                                                                                                                                                                                                                                                                                        Class: TDNA tagged
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25; Conservative
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314 286 1810
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                                                                                                                                                           Unpublished
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DEFINITION
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T60367
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2 GATICITIGCIACTGGCTGCAGCTGCAGCCCCG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Conservative
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Hordeum vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE730257 667 bp mRNA linear EST 15-SEP-2000 601563625F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832999 5',
                                                                                                                              AJ432574 500011 Hordeum vulgare cDNA clone S0001100156E11F1, mRNA
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 667)
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                               Institute of Biotechnology
University of Helsinki
P.O.Box 56 (Vilkinkaari 6A), University of Helsinki FIN-00014,
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National Institutes of Health, Mammalian Gene Collection (WGC)
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Saren,A.-M., Tanskanen,J., Paulin,L. and Schulman,A.H.
Barley asr's
Unpublished
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/clone_lib='800011"
/note="12,15,18 days after pollination"
176 c 142 g 87 t
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                   311 GATCCGGTCCTACAGGCTGCAGCAGCG 343
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2 GATTCTTTGCTACTGGCTGCAGCTGCAGCCCCG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Hordeum vulgare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="S0001100156E11F1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                     AJ432574
AJ432574.1 GI:19521026
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Homo sapiens
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Matches 26; Conservative
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BE730257
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BE730257
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/tissue_type="noise;"
/lab_host="nmelanotic melanoma"
/lab_host="nmelanotic melanoma"
/lab_host="nmelanotic melanoma"
/lab_host="nmelanotic melanoma"
/clone_lib="NIH_MGC_20"
/note="norgan: skin: Vector: poTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRIXAno istes using the following 5'
adaptor: GGCACGAG(G). Sites eslected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
24 a 205 c 225 g 113 t
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.

1 (bases 1 to 687)
Ggilhara; and Murai, K.
Expressed genes in Triticum aestivum
Unpublished
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Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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Pred. No. 1.3e+03;
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National Institute of Genetics
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Plate: LLCM511 row: b column: 08
High quality sequence stop: 667.
Location/Qualifiers
                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                 /mol_type="mRNA"
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/clone="IMAGE:3832999"
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

1. 904

/organism="metraodon.igroviridis"
                                                                                                                                          CNSO4FD7 904 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 106E22 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                        GSS; genome survey sequence.
Tetrackon nigroviridis
Tetrackon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii, Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetrackontiformes;
Tetrackontoidea; Tetrackontidae; Tetrackon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L.L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lb="d"
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/note="Genoscope sequence ID : COBG106BC11LP1~end : T7"
a 210 c 236 g 217 t 4 others
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1 CGATICITIGCIACIGCIGCAGCIGCAGCCCC 33
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/clone="106E22"
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2 hao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Mouse BAC End Sequences from Library RPGI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
Other_GSSs: RCI-24-144M13.TV
Context: Shaying Zhao
Context: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Par: 301 838 0208
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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[bases 1 to 647]
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
Zhao,S., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
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clones are derlived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
avallability, please contact Pieter de Jong (pdejong@mail.cho.org).
clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
pgqe: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Seq primer: 77
class: BAC ends.
    . Constructed by Life Technologies. Note: This Gene Collection (XGC) library." 87 g 139 t
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CH230-100K7.IV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-100K7, genomic survey sequence.
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CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
                                                                                                                                                                         Indels
                                                                                                                       94.4%; Score 17; DB 10; 100.0%; Pred. No. 2.8e+03; tive 0; Mismatches 0;
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    size 1.55 kb. is a Xenopus Garanto
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Contact: Robert Strausberg, Ph.D.

Email: agapbs-refamil.nih, gov

Tissue Procurement: Martha Robert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Asnopus clones from this library are available

through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Seq primer: -400P from Gibco

High quality sequence stop: 412.
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/lab_host="ball0B (phage=resistant)"
/clone_lib="NICHD_XGC_Embl"
/note="vector: pGMV-SFORT6; Site_1: NotI; Site_2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
                                                                                                                                                                                                                                                                                                                                                             /cell_type="Spleen/Brain"
/clone_lib="RPGI-24"
/note="Vector: pTARBACI, Site_l: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The RPCI-24 Mouse Bac Library pass cloned in the pTARBACI cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
library availability, please contact Pieter de Jong (pdejong@mail.cho.org): Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 144 row: M column: 13 Seq primer: SP6 class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                         'organism="Mus musculus"
                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="RPCI-24-144M13"
                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
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/db_xref="taxon:8355"
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BG020388
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RESULT 4 AV319601 ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS

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2 ACAAGGCCAGGACAGAG 18
male testis"
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Mapping of 19032 mouse CDNAs on mouse chromosomes. J. Struct. Placs Genomics 2 pre, L72-L86 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                   Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haramoto, K., Hori, F., Ishil, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Myazaki, A., Nomura, K., Olno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, P., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Muramatsu, M., and Hayashizaki, Y., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEM integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-resegsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,W., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazakl,Y., Muramatsu,M. and Hayashizakl,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                    AV319601 AVIEN full-length enriched, 13 days embryo male testis Mus musculus cDNA clone 6030408J16 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
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Encyclopedia Project of Genome Exploration Research Group in Riken
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                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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On Nov 9, 1999 this sequence version replaced gi:6289434.
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
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/dev_stage="13 days embryo"
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/clone="6030408J16"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                   Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                     Mus musculus
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EST 19-JAN-2001

AUTHORS

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/note="Organ nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES FOR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM2&t2=CM2-NT0169-
291100-525-g11&t3=2000-11-29&t4=1)
Seq primer: pur 18 forward: 2
High quality sequence start: 2
High quality sequence start: 2
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(bases 1 to 201)

Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF925534 200 207 bp mRNA linear EST 19-JAN-200 CM2-NT0169-291100-525-g11 NT0169 Homo sapiens CDNA, mKNA sequence.
BF925534
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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/mol_type="mRNA"
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-hes 17; Conservative
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BF925534
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                    Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Banon, H., Ksaukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Riebi, P., Lerdis, S., Matsuo, T., Mikaldo, I., Pesole, G., Kuchiwa, H., Kami, P., Korlim, L.W., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gaziboldi, M., Gustincich, S., Hill, D., Hofman, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Ring, B., Kingwald, M., Razibolli, J., Mombaetts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, T., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Wonkshaw-Borlis, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Haysshaw-Borlis, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Haysshaw-Borliski, S., Contine, M., Manalla, M., Sanaki, H., Shubala, M., Sanaki, S., Shubala, S., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., And Haysshaw-Borliski, S., Carlin, K., Shubala, S., Shubala, Sh
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S Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hashizume, M., Harashida, K., Hayetsu, M., Hiramanco, K., Hiraoka, T., Hirozane, T., Hori, F., Innotani, K., Ishin, Y., Itch, M., Kaqawa, I., Kawai, T., Katoh, H., Kawai, Y., Kojima, Y., Kondo, S., Konno, H., Kowda, M., Katoh, H., Kawai, K., Nomura, K., Numazaki, A., Murata, M., Okazaki, Y., Saito, R., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Saito, R., Satoh, H., Sasaki, D., Shibata, K., Shinaqawa, A., Shiraki, T., Sasaki, T., Tagami, M., Tagawa, M., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Toya, T., Yasunishi, A., Muramacsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of
Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Ranagawa 230-0405, Japan (E-mail:genome-res@gsc.riken.go.jp,
URI:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cona library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases I to 3005)
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="fatty acid desaturase 2 (MGD|MGI:1930079, GB|NM_019699, evidence: BLASTN, 100%, match=1266)"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'dev_stage="13 days embryo
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URL:http://fantom.gsc.riken.go.jp/
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TITLE JOURNAL

COMMENT

FEATURES

REFERENCE AUTHORS

JOURNAL

TITLE

TITLE JOURNAL

MEDLINE PUBMED REFERENCE

AUTHORS

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Gaps

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5

148 GACAAGGGCAGCACAGAG 165

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/note="Organ placenta_normal; Vector: puc18; Site_1: Smal site_2: Smal; A mini-library was made by cloning products derived from ORSETES POR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 207)

Dias Neto,E., Garcia Correa,R., Verjövski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Fare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=cM2&t2=CM2-GN0166-201100-252-gli&t3=2000-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence store: 207.
                                           BG004130 207 bp mRNA linear EST 24-JAN-2001 CM2-GN0166-201100-525-g11 GN0166 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 bp mRNA linear EST 16-MAY-ssalrgb531327_rev mixed_tissue Salmo salar CDNA, mRNA sequence.
CB513680
CB513680.1 GI:29324906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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94.4%; Pred. No. 4.2e+03;
Live 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0166"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
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                                                                                                                 BG004130.1 GI:12444997
                                                                                                                                                               Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
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Best Local &
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CB513680
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RESULT 7
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Indels

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Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Pases I to 267)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Horl, F., Ishli, Y., Ishlkwa, J., Ishlkwa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagwa, I., Kal, C., Kawai, J., Ishlkwa, T., Itoh, M.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Oazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Saulo, K., Shibata,
'Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suwuki, H., Tagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suwuki, H., Tagawa, A., Takahashi, F., Tominga, N., Toya
'Y., Yano, R., Yasuhishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshiko, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bkoop@uvic.ca
Genome Sciences Centre, BC Cancer Agency CDNA preparation,
sequencing and bioinformatics: Y Butterfield, R Kirkpatrick, J
Asano, N Girn, R Guin, D Lee, S Lee, T Olson, P Pandoh, A Prahbu, D
Smailus, L Spence, J Stott, S Taylor, G Yang, J Schein, S Jones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB007362 RIKEN full-length enriched, 10 day neonate skin Mus musculus cDNA clone 4732477022 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="texon:8030"
//db_xref="texon:8030"
//dbone_lib="mixed_tissue"
//done_lib="mixed_tissue"
//done_lib="mixed_tissue"
//done_lib="mixed_tissue"
//db_xref="vector: prdysport6; library Creator: Research
Genetics , Altantic salmon tissue contributors: Carlo
Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.),
Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery
(Crofton, B.C.), Rachel Roper (University of Victoria)

70 7 9 41 t
                                                                                 Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostomi, Actinopterygli, Neopterygli, Teleostel, Buteleostel, Protacanthopterygli, Salmoniformes, Salmonidae, Salmo.

1 (bases 1 to 245)
GRASP Consortium, Davidson, W.S., Koop, B.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                 http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA
libraries
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                                                                                                                                                                                                                                                                                                                                                                                  Centre for Biomedical Research
University of Victoria
PO Box 3020 SIN CSC, Victoria BC, V8W 3N5, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
                            Salmo salar (Atlantic salmon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 250 472 4067 Fax: 250 472 4075
                                                                                                                                                                                                                                                                                                                                                            Contact: Koop BF
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3B008745.1 GI:8129102
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                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                      SOURCE
                                                                                                                                                                                                                     Email: genome-resigns.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Nishipama.Y., Wastover.A., Itch,M., Nagaoka,S., Sasaki
Carninci.p., Nishipama.Y., Wastover.A., Itch,M., Nagaoka,S., Sasaki
AN., Okazaki,Y., Muramatu.M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
treblaose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad.Sci. U.S.A. 95 (2), 520-524 (1998)
Itch,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'clone_lib="RIKEN full-length enriched, 10 day neonate
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Pred. No. 4.4e+03;
0; Mismatches 1; Indels 0;
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/lab_host="DH10B"
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished
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/organism="Mus musculus"
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/db_xref="taxon:10090"
                                                           Contact: Yoshihide Hayashizaki
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/strain="C57BL/6
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78 c 51
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Best Local Similarity 94.49
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E I (bases 1 to 273)

Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, F., Endo, T., Fukuda, S., Fukuda, J., Raza, H. Baza, H. Rayatan, N., Hirozane, T., Fukuda, S., Fukunishi, Y., Baza, H. Bayatan, N., Hirozane, T., Endi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Ishikawa, T., Itoh, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kodo, S., Kutihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shigmoto, Y., Shinaqawa, A., Shiraki, T., Shibata, K., Shibata, K., Shibata, Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watahashi, F., Tominaga, N., Toya, Y., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Kono, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,T., Westova.A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,T., Muramatsu,M. and Hayashizaki,T.
Thermostabilization and thermoactivation of thermolabile enzymes by
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cDNA. Proc. Natl. Acad. Sci. U.S.A. 55 (2), 520-524 (1998)
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Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Pax: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Carninci,P. and Hayashizaki,Y.
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/lab_host="DH10B"
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/organism="Mus musculus"
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/clone="4732484105"
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/strain="C57BL/6J"
Mus musculus (house mouse)
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BASE COUNT

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Email: genome-res/ggc.riken.go.jp,
URL:http://genome-res/ggc.riken.go.jp,
URL:http://genome-res/ggc.riken.go.jp/
URL:http://genome-sgc.riken.go.jp/
Carninci.p. Nishiyama.Y., Westover.A., Itoh.M., Nagaoka,S., Sasaki
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Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Kawai,J.,
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.ao.ip.
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                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 288)
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/dev_stage="10 days neonate"
/lab_host="DH10B"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
226 GACAAGGGCAGGAGAG 209
                                                                                                                                                                                                                                           BB006387.1 GI:8095786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. .288
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                                                                              RESULT 12
BB006387/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ902923 277 bp DNA linear GSS 05-WAR-2001 RPCI-24-155K10.TJ RPCI-24 Mus musculus genomic clone RPCI-24-155K10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availablity, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://ww.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 155 row: K column: 10
Seq primer: SP6
Class: BAC ends.
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library was cloned in the PTARBACI cloning vector at the
BamHI sites using Mbol partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallai; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 277)
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegage,G., Geerr,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse, BAC End Sequences from Library RPCI-24
                   Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I" 79 c 50 g 73 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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3']. cDNA was cloned into the XhoI and BamHI sites
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                                                                                                                                                            Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                  1; Indels
                                                                                                                                                          Score 16.4; DB 10;
Pred. No. 4.4e+03;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other GSSS: RPCI-24-155K10.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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/clone="RPCI-24-155K10"
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/strain="C57BL/63"
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Mus musculus
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AZ902923.1 GI:13221968
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                                                                                                                                                          Query Match 91.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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SOURCE ORGANISM

KEYWORDS VERSION

REFERENCE AUTHORS

ACCESSION

TITLE JOURNAL

COMMENT

RESULT 11 AZ902923/c DEFINITION

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LOCUS

Query Match

Matches

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BASE COUNT

ORIGIN

source

FEATURES

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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agazose gel electrophoresis. Vector DNA was prepared from a derivative of pWN42 (gil4/32114|gp[AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Department of Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 GACAAGGCCAGGAGAGA 208
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94.4%;
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Best Local Similarity 94.4%;
Matches 17; Conservative
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R41114.1 GI:798730
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Best Local Similarity
Matches 17; Conserv
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                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 312)
Dunn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                           91.1%; Score 16.4; DB 10; Length 288; 94.4%; Pred. No. 4.5e+03; ive 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0273 row: A column: 19
Seg primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus"
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University of Utah Genome Center
University of Utah
        primed with a primer [5'
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High quality sequence stop: 312.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGCIM0273A19"
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                                                                                                                                                                                                                                   75 C
                                                                                                                                                                                                                                                                                                                                     17; Conservative
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Fax: 801 585 7177
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Best Local Similarity
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AZ464111/c
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Fm 302C, Basic Medical Science Building, The Chinese University of
Hong Kong, Shatin, N.T., Hong Kong.
Tel: 8526096874
                                                                                                                                                                                                                                                                  R41114 321 bp mRNA linear EST 16-MAY-1999:
Hk841-f Adult heart, Clontech Homo sapiens cDNA clone k841-f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases I to 321)
Waye, M.M.Y., Chenng, H.K.Y., Lam, W.Y., Law, P.T.W., Lo, A.S.Y., Lui, Y.W.Y., Luk, S.C.W., Tsui, S.K.W., Tung, C.K.C., Yam, N.Y.H., Liew, C.C. and Lee, C.Y.
Gene expression of adult human heart as revealed by random
                                                   Gaps
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Pred. No. 4.6e+03;
0; Mismatches 1; Indels 0;
Score 16.4; DB 28; Length 312;
Pred. No. 4.6e+03;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing of CDNA library
Miami Winter BioTechnol. Symp. Proc. 6, 90 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: b133723@vax.csc.cuhk.hk
Seq primer: GGTGGCGACGACTCCTGGAGCC
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RESULT 15 BY615518 LOCUS

ACCESSION

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

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source
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Kiraido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yadi,K., Tomaru,Y., Hasegawa,Y., Modami,A., Schonbach,C., Golobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbub,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Erusic,V., Chothia,C., Corbani, L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest, J.E., Carimond,S., Gasterland,T., Gariboldi,M., Gassi,C., Godzik,A., Gough,J., Kanaj,H., Kawasawa,Y., Kedzierski,R.M., Jarkson,L.J., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., Jarvis,E.D., Kanaj,A., Kawaji,H., Kawasawa,Y., Redzierski,R.M., Jarvis,E.D., Kondagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons, F.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Naraina,J.M., Sandelin,A., Schonius,J.J., Reed,D.J., Reid,JJ., Ring, B.Z., Ringwald,M., Sandelin,A., Schonider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wanshaw-Boris,A., Yangyi, Javasawa,T., Walki,K., Kawai,J., Rakamura,M., Sandelin,A., Schonius,J., V., Yang,I., Yang,I., Yung,Z., Zavolan,M., Zhu,Y., Zimmer,A., Sandyi,Y., Sardy,I., Yang,Z., Zavolan,M., Zhu,Y., Zimmer,A., Sandyi,Y., Sardy,Y., Sato,K., Shiraka,T., Waki,K., Sasaki,D., Shibata,Y., Itoh,M., Kagawa,I., Myazaki,A., Sakahizuma,M., Yang,I., Yangawa,I., Wayasunishi,A., Yoshino,M., Waterston,R., Jander, K., Shinagawa,A. Yasunishi,A., Yoshino,M., Waterston,R., Lander,R., Shiraki,Y., Sakaki,D., Sakaski,D., Shibata, Sof the mouse transcriptome based on functional annotation of 60,770 full-length conas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-Based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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UKL:http://genome.gsc.riken.go.jp/
Aizawa.K., Akimura.T., Arakawa.T., Carninci,P., Fukuda,S., Hirozane,T., Itoh,W., Kawai,J., Konno,H., Miyazaki,A., Mirata,M., Nakamura,K., Numazaki,R., Ohno,H., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,T. Direct
linear EST 15-DEC-2002
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                      BY615518 RIKEN full-length enriched, visual cortex Mus musculus cDNA clone K330010005 3', mRNA sequence.
BY615518
        mRNA
        349 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                       BY615518.1 GI:26950700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 349)
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        BY615518
                                                                                                                                                                                                                        EST.
                                                DEFINITION
                                                                                                                                                                                                                                                                                                  ORGANISM
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PUBMED
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JOURNAL

COMMENT

TITLE

```
prepare mouse tissues.

Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
arrikan 2-1 Hirosawa, Mako-shi, Saitama 351-0198 Japan ) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="K330010005"
/tissue_type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"
98 c 82 g 79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.4; DB 13; Length 349; Pred. No. 4.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: August 27, 2003, 19:39:58 Job time : 1205.88 secs
                                                                                                                                                                                            Location/Qualifiers
1. .349
                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="c57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACAAGGGCAGGACAGAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GACTAGGGCAGGACAGAG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.1%;
94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 17; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

August 27, 2003, 18:42:00 ; Search time 91.7308 Seconds (without alignments) 450.193 Million cell updates/sec Run on:

1 дасааддусаддасадад 18 US-10-085-612-1 18 Title: Perfect score: Sequence:

IDENTITY_NUC Gapoxt 1.0 Scoring table:

1533700 seqs, 1147125425 residues Searched:

3067400 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_Nh:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PUS06_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 1, Appli	Sequence 13, Appl	Sequence 106890,	Sequence 25159, A	Seguence 10434, A	Sequence 3, Appli	Sequence 3, Appli	Sequence 166368,	Sequence 3, Appli	Sequence 3, Appli	Sequence 20, Appl	Sequence 44, Appl	Sequence 3955, Ap	Sequence 286257,	Seguence 321713,	Sequence 321714,
COMMUNICATION	;	ID	US-10-085-612-1	US-10-146-575-13	US-10-027-632-106890	US-10-027-632-25159	US-10-198-846-10434	US-10-270-336-3	US-09-805-458A-3	US-10-027-632-166368	US-10-146-575-3	US-10-085-612-3	US-09-948-820-20	US-10-146-575-44	US-09-783-590-3955	US-10-027-632-286257	US-10-027-632-321713	US-10-027-632-321714
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	:	Match Length DB	18	29	529	714	1530	119596	172637	745	1345	1345	3881	. 61	299	591	592	592
o¥	Query	Match	100.0	91.1	91.1	91.1	91.1	91.1	91.1	88.9	88.9	88.9	88.9	85.6	85.6	85.6	85.6	85.6
	,	score	18	16.4	16.4	16.4	16.4	16.4	16.4	16	16	16	16	15.4	15.4	15.4	15.4	15.4
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Sequence 105305, Sequence 275296, Sequence 162033, Sequence 162034, Sequence 162034, Sequence 10403, A Sequence 10405, A Sequence 10406, A Sequence 10, Appli Sequence 12, Appli Sequence 21012, A Sequence 21013, A Sequence 21013, A Sequence 21013, A Sequence 21013, A Sequence 69486, A Sequence 5985, A Sequence 5985, A Sequence 5985, A Sequence 5985, A	Sequence 7390, Ap Sequence 7390, Ap Sequence 227843, Sequence 38017, A Sequence 38017, A Sequence 316770, Sequence 70764, A Sequence 72506, A
632-105305 632-15402 632-15403 632-15203 632-16203 632-10403 632-10404 632-10404 632-10404 632-10405 632-10405 632-10405 632-10112 632-1	US-10-027-09488 US-09-864-761-7989 US-10-027-632-38017 US-10-027-632-86427 US-10-027-632-86427 US-10-027-632-70764 US-10-027-632-70764 US-10-027-632-70564
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ALIGNMENTS

RESULT 1

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Sequence 1, Application US/10085612

Publication No. US20030086251A1

GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Guida, Marco
APPLICANT: Guida, Marco
APPLICANT: Petros, William
APPLICANT: Proceedings, James
APPLICANT: Procedulurgh, James
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceutica
TITLE OF INVENTION: Wethods for Evaluating the Ability to Metabolize Pharmaceutica
TITLE OF INVENTION: Compositions Therefor
FILE REFERENCE: 4389-5-C1
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT PELICATION NUMBER: 09/144,367
PRIOR FILING DATE: 2001-02-26
PRIOR PELING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 18; DB 14; Best Local Similarity 100.0%; Pred. No. 18; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-085-612-1
US-10-085-612-1
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1 GACAAGGGCAGGACAGAG 18 RESULT 2 US-10-146-575-13/C g

1 GACAAGGGCAGGACAGAG 18

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Sequence 10434, Application US/10198846
| Bublication No. US20030099974A1
| GENERAL INFORMATION:
| APPLICANT: Lillie, James
| APPLICANT: Lillie, James
| APPLICANT: Lillie, James
| APPLICANT: Mang, Youzhen
| APPLICANT: Wang, Youzhen
| APPLICANT: Wang, Youzhen
| APPLICANT: Steinmann, Kathleen
| APPLICANT: Steinmann, Kathleen
| APPLICANT: Wang, Youzhen
| APPLICANT: Wang, Youzhen
| APPLICANTON: THERRAPY OF BREAST CANCER
| TITLE OF INVENTION: THERRAPY OF BREAST CANCER
| TILLE OF INVENTION: THERRAPY OF BREAST CANCER
| TILLE OF INVENTION: THERRAPY OF BREAST CANCER
| FILE REPRENCE: MRI-049
| CURRENT APPLICATION NUMBER: US/10/198, 846
| CURRENT FILING DATE: 2001-07-18
| PRIOR FILING DATE: 2001-07-18
| WUMBER OF SEQ ID NOS: 14084
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 10434
| LENTH: 1530
                                TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymcrphisms in the Human Genome
FILE REPRENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-89
PRIOR FILING DATE: 1999-09-80
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 74;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.4; I
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.1%; Score 16.4; 94.4%; Pred. No. 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; LOCATION: 897, 1528, 1529, 1530
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-10434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     997 GACGAGGCAGGACAGAG 1014
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 94.4 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human US-10-027-632-25159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-198-846-10434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 25159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Devid G.

TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFRENCE: 108827.123

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1200-02-24

PRIOR FILING DATE: 1299-11-13

PRIOR APPLICATION NUMBER: US 60/165,363

PRIOR FILING DATE: 1999-11-13

PRIOR APPLICATION NUMBER: US 60/166,368

PRIOR PILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
Sequence 13, Application US/10146575;
Publication No. US20030059800A1
GENERAL INPORMATION:
APPLICANT: Liother, Jay
APPLICANT: Gindo, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REPRENENCE: SEQ.12P
CURRENT APPLICATION NUMBER: US/10/146,575
CURRENT FILING DATE: 2002-05-14
FRIOR APPLICATION NUMBER: US/09/144,367
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 58
SOFTMARE: FASTSEQ for Mindows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.1%; Score 16.4; D 94.4%; Pred. No. 1e+0 tive 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 106890, Application US/10027632
; GENERAL INFORMATION:
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity 94.43
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: H. sapiens
US-10-146-575-13
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; ORGANISM: Human
US-10-027-632-106890
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LENGIH: 29
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GENERAL INVENTATION:

GENERAL INVENTATION: David G.

TITLE OF INVENTION: David G.

TITLE OF INVENTION: Delincification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10887.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2000-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/167,353

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-09

SOUPWARE: FRASESQ for Windows Version 4.0

SEQ ID NO 166368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.9%; Score 16; DB 13; Length 745; 88.9%; Pred. No. 1.2e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
CURRENT APPLICATION NUMBER: US/10/146,575
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US/09/144,367
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
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Mismatches 1;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 GTCAAGGGCAGGACAGRG 29
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (0)...(0) US-10-146-575-3
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US-10-027-632-166368
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US-10-085-612-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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Sequence 3, Application US/09805458A
Sequence 3, Application US/09805458A
Sequence 3, Application US/09805458A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000722
CURRENT APPLICATION NUMBER: US/09/805,458A
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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                                                                   Sequence 3, Application US/10270336
Publication No. US20030074678a1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SIGNATED HURAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REPERBACE: CL001146COM
CURRENT APPLICATION NUMBER: US/10/270,336
CURRENT APPLICATION NUMBER: US 60/270,873
PRIOR PILING DATE: 2001-02-05
COUPRED: CS EQU ID NOS: 7
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Best Local Similarity 94.4%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 119596
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US-10-027-632-166368/c
; Sequence 166368, Application US/10027632
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; LOCATION: (1)...(119596)
; OTHER INFORMATION: n = A,T,C or G
US-10-270-336-3
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) LOCATION: (1)...(172637)

) CHER INFORMATION: n = A,T,C or G

02-09-805-458A-3
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Best Local Similarity 94.4%;
Matches 17; Conservative (
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US-09-805-458A-3
                                                            US-10-270-336-3
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Sequence 3955, Application US/09783590
Fatent No. US20020110850A1
GENERAL INDEMATION.
SAPLICANT: DAIllon, Partick J.
APPLICANT: DAIllon, Partick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Hadong
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
TILLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE PERFERNCS: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT APPLICATION NUMBER: 08/420,856
FRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3955
                                                                                                                                                                                                                                                                                                                                                                                  85.6%; Score 15.4; DB 14; Length 19; 94.1%; Pred. No. 3.2e+02; tive 0; Mismatches 1; Indels
  APPLICANT: Lichter, Jay
APPLICANT: Gildo, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FITLE REPERENCE: SEO-12
CURRENT APPLICATION NUMBER: US/10/146,575
CURRENT PILING DATE: 2002-05-14
FRIOR APPLICATION NUMBER: US/9/144,367
FRIOR PILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 19
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (23)
OTHER INFORMATION: n equals a,t,g, or c
NAME/RET: misc feature
LOCATION: (45)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
MME/KEY: misc feature
LOCATION: (8)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OOTHER THYORWATION: n equals a,t,g,
NAME/KET: misc feature
LOCATION: (131)
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Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: H. sapiens
US-10-146-575-44
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                                                                                             APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Petros, William
APPLICANT: Petros, William
APPLICANT: Octyin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
TITLE OF INVENTION: Compositions Therefor
TITLE OF INVENTION: COMPOSITIONS (1895,612
CURRENT FILING DATE: 2002-02-26
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Version 3.0
SEQ ID NO 3
LENGTH: 1345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 14; Length 1345;
Pred. No. 1.1e+02;
1; Mismatches 1; Indels (
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US-09-948-820-20/c
| Sequence 20, Application US/09948320
| Publication No. US20030050460A1
| GENERAL INCORMATION:
| APPLICANT: Ni et al.
| TILLE DF INVENTON: 31 Human Secreted Proteins
| TILLE REFERENCE: P2034P1
| CURRENT FILING DATE: 2001-09-10
| PRIOR PILING DATE: 2001-09-10
| PRIOR PILING DATE: 1999-11-09
| PRIOR PILING DATE: 1999-11-09
| PRIOR PILING DATE: 1999-11-09
| PRIOR FILING DATE: 1999-11-09
| PRIOR FILING DATE: 1998-11-12
| NUMBER OF SEQ ID NOS: 115
| SOFTWARE: PARENTING DATE: 1998-11-12
| NUMBER OF SEQ ID NOS: 115
| LENGTH: 3881
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US-10-146-575-44
; Sequence 44, Application US/10146575
; Publication No. US20030659800A1
; GENERAL INFORMATION:
Sequence 3, Application US/10085612 Publication No. US20030096251A1 GENERAL INFORMATION:
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.9
Best Local Similarity 88.9
Matches 16; Conservative
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US-09-948-820-20
                                                                         APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-085-612-3
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERSENCE: 108827:129
FILE REPERSENCE: 108827:129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PLILNG DATE: 2000-04-20
PRIOR PLILNG DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1090-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PLILNG DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
SPRIOR FILING DATE: 1999-08-09

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: August 27, 2003, 21:14:03 Job time : 92.7308 secs
                Sequence 321713, Application US/10027632 GENERAL INFORWATION:
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US-10-027-632-286257/C

| Sequence 286257, Application US/10027632
| GENERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Telentification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: POLYMORPHISMS in the Human Genome
| TITLE OF INVENTION: POLYMORPHISMS in the Human Genome
| FILE REFERENCE: 108827.129
| CURRENT APPLICATION NUMBER: US 60/218,006
| PRIOR FILING DATE: 2000-04-30
| PRIOR FILING DATE: 2000-04-20
| PRIOR PRILING DATE: 2000-04-20
| PRIOR PAPLICATION NUMBER: US 60/185,218
| PRIOR PLILING DATE: 2000-03-29
| PRIOR PLILING DATE: 1999-11-23
| PRIOR PLILING DATE: 1999-11-23
| PRIOR PLILING DATE: 1999-09-28
| PRIOR PLILING DATE: 1999-09-28
| PRIOR PLILING DATE: 1999-09-28
| PRIOR PLILING DATE: 1999-09-08-09
| PRIOR PLILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.6%; Score 15.4; DB 10; Length 299; Best Local Similarity 88.9%; Pred. No. 2.4e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 591;
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Pred. No. 2.3e+02;
); Mismatches 1;
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SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 286257
LENGTH: 591
                                                                                                                                                                                                                                                                                                          LOCATION: (214)
OTHER INFORMATION: n equals a,t,g, or c MAME/RET: misc feature
LOCATION: (267)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KET: misc feature
LOCATION: (271)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: n equals a,t,g, or c US-09-783-590-3955
                                                                            LOCATION: (132)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                             LOCATION: (204)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature
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303 GAAAAGGGCAGGACAGA 287
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Best Local Similarity 94.1%;
Matches 16; Conservative
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US-10-027-632-286257
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RESULT 15 US-10-027-632-321713

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

000	Anginet	77 2003 18:00:44
	in fine	(Without alignments) (372.452 Million cell
Title: Perfect score: Sequence:	US-10 34 1 cge	-10-085-612-2 cgattctttgctactggctgcagctgcagccccg 34
Scoring table:	IDEN	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711	711 segs, 20454813386 residues
Total number of	hits	satisfying chosen parameters: 5777422
Minimum DB seq Maximum DB seq	length: length:	n: 0 h: 200000000
Post-processing		Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database .	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	GenEmbl:* gb_ba:* gb_ba:* gb_ba:* gb_om:* gb_om:* gb_om:* gb_om:* gb_pat:* gen_pat:* gen_pa

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

	Description	472122 Seque	Homo	AC069294 Homo sapi	Ношо	Seque	Seque	AX472216 Sequence	AX472217 Sequence	AX472218 Sequence	AX706964 Sequence	Seque	AF280107 Homo sapi	AX472125 Sequence	AX472244 Sequence	AC141417 Papio anu	AX472134 Sequence	AX472132 Sequence	AX4/2133 Sequence	AX472235 Sequence	AA4/2230 Sequence	AA/00302 Sequence	ACOUSTO HOMO Sapi	AC095225 Rattus no	AC104927 Mus muscu	Mus musc	Rattus	Rattus	AC129000 RALLUS 110	ECHOS CE	HOMO S	AR142139 Sequence	Sequen	AR222893 Sequence	AX421253 Sequence	D11131 Homo sapien	AF329900 Homo sapi	Homo sapi	BV031220 S212P6047	Homo s	Human	Homo	Homo	Homo sa	
		AX472122	AF325929	AC069294	AF315320S4	AX472123	AX472124	AX472216	AX472217	AX472218	AX706964	AX707894	AF280107	AX472125	AX472244	AC141417	AX472134	AX472132	AX472133	AX472235	AX4 / 2236	A&/06962	AC107832	AC095225_0	AC104927	AC129544	AC106955	AC128973	ACLASO00	ACUSOS13	AF181105	AR142139	AR142140	AR222893	AX421253	HUMCYP3A4	AF329900	AF185589	L BV031220	AC016679	HSA213H19	AC073227	AC090810	AC067832	
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646	Query	100.0	100.	100.0	97.	97.	97.	97.	97.	97.	97.	97.	97.1	92.	92.4	90.6	81.	81	8	81.	7.18	21.5	81.2	67.6	9.79	67.6	67.6	67.6	01.0	0.70	. 29	67.	67.	67.	67.	67.	67.	67.	92	65	65	92	92	65.	
	Score	34	34	34	33	33	33	33	33	33	33	33	33	<u>~</u>	÷.	ö	7	۲.	٠.	۲.	٠,	٠,	27.0	. (4	23	23	23	23	2 6			22.8													
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ALIGNMENTS

G-2002		omi;	,
PAT 09-AUG-2002		Euteleost ; Homo.	olymorphic
linear		<pre>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</pre>	1 Hustert,E., Haberl,M. and Wojnowski,L. Identification of the genetic determinants of the polymorphic cyp3a5 expression
p DNA	53775.	Craniata; Catarrhin	owski,L. determina
830 bp	Sequence 113 from Patent W002053775. AX472122 AX472122.1 GI:22207163	Chordata; Primates;	l. and Wojn we genetic
: :	Sequence 113 from Paten AX472122 AX472122.1 GI:22207163	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;	, Haberl, Mition of the pression
AX472122	Sequence 1 AX472122 AX472122.1	Homo sapiens Homo sapiens Eukaryota; Me Mammalia; Eu	1 Hustert,E., Haber Identification of Cyp3a5 expression
AX472122 LOCUS	DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the
                                                                                                                                                                                                                                       PRI 09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Britheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 123778)
Sulston.J.E. and Waterston,R.
                                                                                                                                                                                                                     ACU69294 123778 bp DNA linear PRI 09-MA'
Homo sapiens BAC clone RP11-757A13 from 7, complete sequence.
ACU69294
                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center
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Bielicki,L. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-757A13
                                           Indels
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                          1360 CGATTCTTTGCTACTGGCTGCAGCTGCAGCCCCG 1393
                    Pred. No. 0.0012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                 1 CGATICITIGCIACIGGCIGCAGCIGCAGCCCCG
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                                           Mismatches
100.08; Li
                                                                                                                                                                                                                                                                                                       AC069294.5 GI:13112210
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Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                             34; Conservative
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                    Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                              ACCESSION
VERSION
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AUTHORS
TITLE
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Kuehl, P.M., Zhang, J., Lin, Y., Watkins, P., Maurel, P., Daly, A.,
Kuehl, P.M., Zhang, J., Lin, Y., Watkins, P., Maurel, P., Daly, A.,
Wrighton, S., Hall, S., Relling, M., Schuetz, J., Brimer, C., Yasuda, K.,
Storm, S., Thummel, K.,
Schuetz, E. and Boguski, M.

Direct Submission
Submission
Submission
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI 06-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1612)

Kuehl, P., Zhang, J., Lin, Y., Lamba, J., Assem, M., Schuetz, J., Watkins, P.B., Daly, A., Wrighton, S.A., Hall, S.D., Maurel, P., Thummel, K., Brimer, C., Yasuda, K., Venkataramanan, R., Storm, S., Thummel, K., Boguski, M. S. and Schuetz, E. Sequence diversity in CYB3A promoters and characterization of the genetic basis of polymorphic CYP3A5 expression

Nat. Genet. 27 (4), 383-391 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/Mote="2 base mismatch and 2 base insertion compared to
GenBank Accession Number 874700"
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1612 bp DNA linear PRI 06-D. Homo sapiens cytochrome P450 (CYP3AP1) pseudogene, CYP3AP1*1 allele, partial sequence, including promoter region. AF325929
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                                                                                                                                                                                                                                       Length 830;
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               Patent: WO 02053775-A 113 11-JUL-2002;
BPIDAUROS BIOTECHNOLOGIE AG (DE)
Location/Qualifiers
1. .830
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                                                                                                                                                                                                                                     Score 34;
Pred. No. 0
                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/gene="CYP3AP1"
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/gene="CYP3AP1"
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 EST AW890805 (NID:98055010)"
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23524. 23650
2461. 23650
2461. 2.4717
/rpt_family="MIR"
24820. 25131
           12025. .12034
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12509. .14044
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15354. .11634
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2357. .12634
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15357. .15634
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15373. .15634
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19623. .19743
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26402. .26483
/rpt_family="L1"
26485. .26797
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27787. .27913
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/rpt_family="MIR"
30396. .30596
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/rpt_family="Alu"
28815. .28939
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/rpt_family="Alu"
14137. .15361
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/rpt_family="L1"
20499. .21923
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Tpt_family="L2"
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/rpt_family="L1"
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'rpt_family="L1"
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                                                                                                                               The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa. K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
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note="similar to EST A1377273 (NID:94187126) te65b04.x1"
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                                                                                                                                                                                                                                                                                                                       The clone sequenced to the right is GS1-259H13, 200 bp overlap; the clone sequenced to the left is GPn-32440H8, 200 bp overlap. Actual start of this clone is at base position 59560 of GTD-32440H8; actual end is at base position 25744 of GS1-259H13.
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Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.uih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                               The sequence from base position 113692 to 114784 is derived from single plasmid subclone. Assembly in this region is supported by HindIII digest information.
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2453. 2756
/rpt_family="Alu"
3874. 4033
/rpt_family="MER1_type"
10188. 10513
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NEIGHBORING SEQUENCE INFORMATION:
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/clone_lib="RPCI-11"
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/rpt_family="ERV1"
11537. .11822
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note≕"similar to
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note="similar to
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11814. .12038
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rpt_family="Alu"
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rpt_family="Alu"
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pt_family="L2"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Identification of the genetic determinants of the polymorphic cyp3a5 expression
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cypsa5 expression
Patent: WO 02053775-A 115 11-JUL-2002;
EPIDAUROS BIOTECHNOLOGIE AG (DE)
Location/Qualifiers
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33; Conservative 0; Mismatches 0;
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BPIDAUROS BIOTECHNOLOGIE AG (DE)
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176 c 236 g 187
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Rominidae; Homo.
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Finta,C. and Zaphiropoulos,P.G.
The human cytochrome P450 3A locus. Gene evolution by capture of
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Finta,C. and Zaphiropoulos,P.G.

Finta,C. and Zaphiropoulos,P.G.

Finta,C. and Zaphiropoulos,P.G.

Finta,C. and Zaphiropoulos,P.G.

Submisted (23-0CT-2000) Department of Biosciences, Karolinska
Institute, NOVUM, Huddinge 14157, Sweden

Location/Qualifiers

Location/Qualifiers

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Anologous="Toologous"

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Identification of the genetic determinants of the polymorphic cyp3a5 expression
Patent: WO 02053775-A 114 11-JUL-2002;
EPLDAUROS BIOTECHNOLOGIE AG (DE)
Location/Qualifiers
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a 176 c 236 g 18:
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/clone="CITB BAC 128D24"
246. .316
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AF280107 174832 bp DNA linear PRI 26-MAR-2001 Home sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial eds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds.
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Methods for the treatment of cancer with irinotecan based on CYP3A5
Patent: WO 03013534-A 662 20-PEB-2003;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
1. 96960
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Methods for treatment of cancer using irinotecan based on UGTIA1
Patent: WO 03013354-A 662 20-FEB-2003;
Bpidauros Bottechnologie AG (DE)
Location/Qualifiers
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97.1%; Score 33; DB 6; Length 96960;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 33; Conservative 0; Mismatches 0; Indels
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a 19882 c 20450 g 29221 t.
                           Sequence 662 from Patent WO03013534..
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AF280107
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                                                                                                                               PAT 09-AUG-2002
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Identification of the genetic determinants of the polymorphic
gppa55 expression
Patent: WO 02053775-A 209 11-JUL-2002;
EPIDAUROS BIOTECHNOLOGIE AG (DE)
                                                                                                                                                                                                                                                                                                               Hustert,E., Haberl,M. and Wojnowski,L.
Identification of the genetic determinants of the polymorphic
cypas5 expression
Patent: WO 02053775-A 208 11-JUL-2002;
BRIDAUROS BIOTECHNOLOGIE AG (DE)
Location/Qualifiers
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Sequence 209 from Patent WO02053775.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
t 175 c 237 g 188
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
a 177 c 237 g 18
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Best Local Similarity 100.0
Matches 33; Conservative
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ORGANISM

REFERENCE AUTHORS

MEDLINE PUBMED REFERENCE AUTHORS

JOURNAL

TITLE

ACCESSION VERSION

KEYWORDS

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/translation="MDLIPNLAVETWLLLAVSLVLLYLYGTRTHGLFKRLGIPGPTPL
PLLGNVLSYRQGLWKFDTECYKKYGKMGTYEGQLPVLAITDPDVIRTVLVKECYSVF
                                                                                                      VVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIGMRFALM
NMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA"
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RREAETGKPVTLKHVFGAYSMDVITSTSFGVSIDSLNNPQDPFVENTKKLLRFNPLDP
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IDTVLPNKAPPTYDTVLQLEYLDMYNNFİLRLFPVAMRLERVCKKDVEINGMFIPKGV
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REAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFVENTKKLLRFDFLDP
                        PLSITVEPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDTOKHRVDFLOLMI
                                                DSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATHPDVQQKLQEE
                                                                                 :DAVLPNKAPPTYDTVLOMEYLDMVVNETLRLFPLAMRLERVCKKDVEINGMFIPKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="molipnlaverwillavslillylgtrthglekkigipgpppl
PFLGNALSFRKGYWTFDMECYKKYRKVWGIYDCQQPWLAITDPDMIKTVLVKECYSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVLSIKVFPFLTPILEALNITVFPRKVISFLTKSVKQIKEGRLKETQKHRVDFLQLMI
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/note="ps2_1; similar to CYP3A5 exon 1" 150277. 150370.
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.73442. .>173541)
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125691. .125790,128465. .128578,128839. .128927,
130198. .130346,131422. .131549,132569. .132635,
25215. .135375,136850. .137076,138137. .138299,
140516. .141067)
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join(16520. 166290,163908. .170001,171536.
173442. .>173541)
/gene-"cyp3a5"
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                                                                                                                                                             93618. .93688
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/note="ps1_2; similar to CYP3A7 exon 2"
110906. .141067
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join(62037. 62107,66034. 66127,68039. 68091,73420. .73519,
15874. .75987,76533. .76741,77677. .7755,78851. .78978.
9666. .79732,82094. .82254,83842. .84068,85128. .85290,
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/db_xref="G1:11177456"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MalipDiaMETWLLLAVSLVLLYLYGTHSHGLFKKLGIPGPPL
PFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAITDPDMIKTVLVKECYSVF
TNRRPFGPVGFMKSALSIAEDEEWKRLRSLLSPFTSGKLKEWYPIIAQYGDVLVRNL
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                                                                                                                                                                                                                                                                                                                                      Genomic organization of the human CYP3A locus: identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (20-JUN-2000) EPIDAUROS Biotechnologie AG, Am Neuland 1,
Bernried 82347, Germany
Location/Qualifiers
                                                                                                                               Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases I to 174832)

2 (Dases, I. to 174832)

2 (Ballner, K., Biselt, R., Hustert, E., Arnold, H., Koch, I., Haberl, M., Deglmann, C.J., Burk, O., Buntefuss, D., Escher, S., Bishop, C., Koebe, H.-G., Brinkmann, U., Klenk, H.-P., Kleine, K., Meyer, U.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to sequence deposited in AC011904 and to AC005020; cytochrome P450 IIIA locus sequence" complement(-1. 1862)
/gene="CYP2A43" complement(join(<1862. 1961,6932. 6984,9558. 9651, 17918. 18091).
/product="cytochrome P450 polypeptide 43" complement(join(<1862. 1961,6932. 6984,9558. 9651,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cases 1 to 174832)
Gellner, K., Eiselt, R., Hustert, E., Arnold, H., Koch, I.,
Deglmann, C.J., Burk, O., Haberl, M., Buntefuss, D., Escher, S.,
Bishop, C., Koebe, H. G., Brinkmann, U., Klenk, H. -P., Kleine, K.
Meyer, U.A. and Wojnowski, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="cytochrome P450 polypeptide 43"
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/hote="hps3.1; similar to CYP3A43 exon 1"
61934 . B843.2
/gene="CYP3A4"
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                                                                                                                                                                                                                                                                                                                                                           new, inducible CYP3A gene
Pharmacogenetics 11 (2), 111-121 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="subfamily IIIA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="BAC22300"
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                     GI:11177452
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/gene="CYP3A4"
                                                                           Homo sapiens (human)
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gene mRNA

CDS

source

FEATURES

gene mRNA

CDS

TITLE JOURNAL

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Submitted (27-MAX-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, 67 73019, USA ON May 21, 2003 this sequence version replaced gi:30103048.
                                                                                                                                                                                                                                                                     Submitted (14-MAR-2003) Department Of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
1 (bases 1 to 174004)
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/db_xref="taxon:9555"
/db_xref="taxon:9555"
/clone="rp41-443b7"
/clone="rp41-443b7"
/clone=lib="RRCI - 41 Male (Olive) Baboon BAC Library"
/ 35579 c 35808 g 52374 t 403 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30.8; DB 2; Length 174004;
Pred. No. 0.024;
0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                      2 (bases 1 to 174004)
Prescott,A., Slegfried,M., DiRienzo,A. and Roe,B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                    Prescott, A., Siegfried, M., DiRienzo, A. and Roe, B.A. Direct Submission
                                                                                                                                                Prescott, A., Siegfried, M., DiRienzo, A. and Roe, B.A. Papio anubis BAC Clone rp41-443b7
Unpublished
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1. 174004
/organism="Papio anubis"
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                  HTG; HTGS_PHASE1; HTGS_DRAFT.
Papio anubis (olive baboon)
Papio anubis
  AC141417.7 GI:30962786
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Best Local Similarity 94.1%;
Matches 32; Conservative
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                    PAT 09-AUG-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Identification of the genetic determinants of the polymorphic grants expression
Payba5 expression
Patent: WO (0.053775-A 235 11-JUL-2002;
EPIDAUROS BIOTECHNOLOGIE AG (DE)
                                                                                                                                                                                                                   Hustert,E., Haberl,M. and Wojnowski,L.
Identification of the genetic determinants of the polymorphic cyp3a5 expression
Patent: WO 02053775-A 116 11-JUL-2002;
EPIDAUROS BIOTECHNOLOGIE AG (DE)
Location/Qualifiers
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Sequence.116 from Patent W002053775.
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/db_xref="taxon:9606"
a 176 c 236 g 187
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/db_xref="taxon:9606"
a 177 c 237 g 18
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                                                                             AX472125.1 GI:22207166
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ilarity 97.0%;
Conservative (
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Human CYP3A5 gene

Title: Perfect score: Sequence:

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Scoring table:

Searched:

Database

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/standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytochrome P450; CYP3A4; CYP3A5; glutathione S-transferase;
GSYMI; breast cancer; therapy; chemotherapeutic agent; variant;
drug-drug interaction; drug adverse effect; anti-cancer agent; SNP;
enzyme; single nucleotide polymorphism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytochrome P450 (CYP) 3A5 polymorphic variant DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                         AAZ57019
AAZ57020
ABK68745
AAD41242
AAD36213
AAD41239
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ABZ81775
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AAD43350
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ABL22064
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792
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Synthetic.
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variation
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AAD45761
 Human cytochrome P
Human CYP3A5 gene
DNA sequence of hu
Human cytochrome P
Human CYP3A5 gene
Human CYP3A5 gene
Human CYP3A5 gene
Human CYP3A5 gene
                                                                                         August 27, 2003, 17:59:19; Search time 264.808 Seconds (without alignments) 346.595 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/ SIDEAL/Gradata_Geneseq_Geneseque_embl_NAL1990_DAT:*
/ SIDEAL/Gradata_Geneseq_Geneseque_embl_NAL1991_DAT:*
/ SIDEAL/Gradata_Geneseq_Geneseque_embl_NAL1991_DAT:*
/ SIDEAL/Gradata_Geneseq_Geneseque_embl_NAL1991_DAT:*
/ SIDEAL/Gradata_Geneseq_Geneseque_embl_NAL1994_DAT:*
/ SIDEAL/Gradata_Geneseq_Geneseque_embl_NAL1996_DAT:*
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/ SIDEAL/Gradata_Geneseq_Geneseque_embl_NAL1991_DAT:*
/ SIDEAL/Gradata_Geneseq_Geneseque_embl_NAL1999_DAT:*
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           GenCore version 5.1.6
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34
1 cgattctttgctactggctgcagctgcagcccg 34
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Best Local Si
Matches 34,
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                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
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                                                                                                                                                             The invention relates to a nucleic acid molecule comprising at least one base variation from human cytochrome P450 (CVF) 344 or CVP3A5 sequence.

Nucleic acid molecules of the invention are useful for identifying polymorphisms associated with CYP3A4, CYP3A5 or glutathione S-transferase (GST) MI substrates which influence breast cancer treatments. They are also useful in diagnostic purposes to identify individuals having a polymorphic genotype which influence the outcome of breast cancer. The polymorphisms detected are used to streat cancer. The polymorphisms detected are used to streat cancer and the selection of chemotherapeutic agents used to treat cancer. The polymorphisms detected are used to stread metabolism of CYP3A4, CYP3A5 or GSTMI substrates, potential drug-drug interactions, drug adverse effects, likelihood of successful clinical cutome following treatment with anti-cancer agents such as cisplatin, cyclophosphanide and/or BCNU. The present sequence is human CYP3A5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
AIDS; African American; forensic marker; pharmacological; cytostatic;
antidiabetic; anti-HIV; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                   Petros WP, Vredenburgh JJ, Colvin OM, Marks JR;
                                                                              New nucleic acid molecule useful for identifying polymorphisms associated with CYP344, CYP345 or GSTM1 substrates which influence breast cancer treatments, comprises at least one base variation from human CYP9340 or CYP935 sequence
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                                                                                                                                                                                                                                                                                                                                                                  Length 34;
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Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 34; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                          Sequence 34 BP; 4 A; 12 C; 9 G; 9 T; 0 other;
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                                                                                                                                          Claim 9; Page 12; 41pp; English
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2001US-262859P.
2001EP-0118884.
2001US-312825P.
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                                                         WPI; 2002-691652/74.
DNA SCI INC.
UNIV DUKE.
                                   Guida M, Hall J,
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16-AUG-2001;
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28-DEC-2000;
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The present invention relates to a new CYP3A5 polynucleotide encoding a polypeptide, where the polynucleotide is capable of hybridising to a CYP3A5 gene. The invention is useful in an in vitro method for identifying a polymorphism. The invention is also useful for useful for identifying a polymorphism. The invention is also useful for useful for diagnosing a disorder related to the presence of a molecular variant of cripax5 or susceptibility to such a disorder, where the disorder is cancer, or diseases including cardiovascular diseases, diabetes and AIDS. The invention can further be used for the preparation of a diagnostic composition for diagnosing a disease in a subject having a genome composition for diagnosing a disease in a subject having a genome composition are included of the CYP3A5 gene, where the subject is an African American. The molecules of the invention are as forensic markers and in pharmacological studies. The present nucleic acid sequence represents a genomic DNA sequence that contains a region in which a polymorphism of the human CYP3A5 gene was detected.
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                                 Novel CYP3A5 polynuclectide useful for diagnosis and treatment of cancer, cardiovascular diseases, diabetes and AIDS, and for identifying polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New transgenic non-human animal expressing a foreign polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 24; Length 830; 100.0%; Pred. No. 0.0012; ive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 830 BP; 229 A; 176 C; 239 G; 186 T; 0 other;
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                                                                                                                                                                                                                                                                 Claim 1; Figure 4; 138pp; English.
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WPI; 2002-583628/62
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used for assessing the behaviour and/or metabolism of a drug in another animal and which expresses a foreign polypeptide associated with drug behaviour and/or metabolism. The invention also comprises a nucleic acid construct for use in producing the above transgenic non-human animal and a method of assessing the metabolism and/or behavior of a drug in animal of interest, comprising administering test agent to the transgenic animal and conducting analytical tests to determine drug metabolism and/or behaviour. The transgenic animal is useful in studying construct is useful in producing the above transgenic animal and the methods are used for producing, the above transgenic animals construct is useful in producing the above transgenic animals of the invention are serum albumin; alpha-acidic glycoprotein; cytochrome P450 (CPT) utilizine diphosphoglucuronosyl transferase (UGT); multidrug resistance proteins and (MRP's). The present sequence represents a DNA sequence used to create a transgenic animal within the scope of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytochrome P450; CYP3A4; CYP3A5; glutathione S-transferase; polymorphism; GSTM1; breast cancer; therapy; chemotherapeutic agent; drug-drug interaction; drug adverse effect; anti-cancer agent;
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Best Local Similarity 100.0%;
Matches 34; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                       invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer, cardiovascular diseases, diabetes and AIDS, and for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, CYP3A5, polymorphism, cancer, cardiovascular disease, diabetes, AIDS, African American, forensic marker, pharmacological, cytostatic; antidiabetic; anti-HIV; gene therapy, ds.
(GST) M1 substrates which influence breast cancer treatments. They are
              also useful in diagnostic purposes to identify individuals having a polymorphic genotype which influence the outcome of breast cancer treatments and the selection of chemotherapeutic agents used to treat breast cancer. The polymorphisms detected are used to screen altered metabolism of CYD3A4, CYP3A5 or GSTM1 substrates, potential drug-drug interactions, drug adverse effects, likelihood of successful clinical outcome following treatment with anti-cancer agents such as cisplatin, cyclophosphamide and/or BCNU. The present sequence is human CYP3A5
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100.0%; Pred. No. 0.0017;
7ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                             Sequence 34 BP; 5 A; 12 C; 8 G; 9 T; 0 other;
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29-DEC-2000; 2000US-258952P.
16-JAN-2001; 2001EP-0100172.
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16-AUG-2001; 2001EP-0118884
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Best Local Similarity 100.
Matches 33; Conservative
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                                                                                                                                                                          wild-type DNA fragment
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                African American. The molecules of the invention are as forensic markers and in pharmacological studies. The present nucleic acid sequence represents a genomic DNA sequence that contains a region in which a polymorphism of the human CFPARS gene was detected.
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comprising a variant allele of the CYP3A5 gene, where the subject is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, CXP3A5; polymorphism; cancer; cardiovascular disease; diabetes; AIDS; African American; forensic marker; pharmacological; cytostatic; antidiabetic; anti-HIV; gene therapy; ds.
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                                                                                                                                                       Match 97.1%; Score 33; DB 24; Length 830; Local Similarity 100.0%; Pred. No. 0.0029; les 33; Conservative 0; Mismatches 0; Indels
                                                                                                                     Sequence 830 BP; 231 A; 176 C; 236 G; 187 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CYP3A5 gene polymorphic DNA sequence #3.
                                                                                                                                                                                                                                                            549 CGATTCTTTGCTACTGGCTGCAGCTGCAGCCCC 581
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2000US-258952P.
2001EP-0100172.
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16-AUG-2001; 2001US-312825P
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29-DEC-2000;
16-JAN-2001;
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Matches
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The present invention relates to a new CYP3A5 polynucleotide encoding a polypeptide, where the polynucleotide is capable of hybridising to a CYP3A5 gene. The invention is useful in an in vitro method useful for identifying a polymorphism. The invention is also useful for useful for identifying a polymorphism. The invention is also useful for useful for diagnosing a disorder related to the presence of a molecular variant of a CYP3A5 or susceptibility to such a disorder, where the disorder is cancer, or diseases including cardiovascular diseases, diabetes and AIDS. The invention for diagnosing a disease in a subject having a genome composition for diagnosing a disease in a subject having a genome composition a variant allele of the CYP3A5 gene, where the subject is an African American. The molecules of the invention are as forensic markers and in pharmacological studies. The present nucleic acid sequence represents a genomic DNA sequence that contains a region in which a polymorphism of the human CYP3A5 gene was detected.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes; AIDS; African American; forensic marker; pharmacological; cytostatic; antidiabetic; anti-HIV; gene therapy; ds.
                                                                                                                       Gaps
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Sequence 830 BP; 231 A; 176 C; 236 G; 187 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CYP3A5 gene polymorphic DNA sequence #30.
                                                           Score 33; DB 24;
Pred. No. 0.0029;
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100.0%; Pred. No. v.
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2001US-262859P
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2001US-312825P
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                               Query Match
Best Local Similarity 100.00
Best Local 33; Conservative
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28-DEC-2000;
29-DEC-2000;
16-JAN-2001;
18-JAN-2001;
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16-AUG-2001;
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ABK99499
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The present invention relates to a new CYP3A5 polynucleotide encoding a polypeptide, where the polynucleotide is capable of hybridising to a CYP3A5 gene. The invention is useful in an in vitro method for identifying a polymorphism. The invention is also useful for useful for diagnosing a disorder related to the presence of a molecular variant of a CYP3A5 or susceptibility to such a disorder, where the disorder is cancer, or diseases including cardiovascular diseases, diabetes and AIDS. The invention can further be used for the preparation of a diagnostic composition for diagnosing a disease in a subject having a genome composition for diagnosing a disease in a subject having a genome composition and in pharmacological studies of the invention are as forensic markers and in pharmacological studies. The present nucleic acid sequence represents a genomic DNA sequence that contains a region in which a polymorphism of the human CYP3A5 gene was detected.
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                                                                                                                                                                                                                           Human, CYP3A5, polymorphism; cancer; cardiovascular disease; diabetes;
AIDS, African American; forensic marker; pharmacological; cytostatic;
antidiabetic; anti-HIV; gene therapy; ds.
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100.0%; Pred. No. 0.0029;
live 0; Mismatches 0;
                                                                                                                                                                                  Human CYP3A5 gene polymorphic DNA sequence #32
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                                                                                                                                                                                                                                                                                                                                          Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes; AIDS; African American; forensic marker; pharmacological; cytostatic; antidiabetic; anti-HIV; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                 gene polymorphic DNA sequence #31.
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Pred. No. 0.0029;
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1 CGALICITIGCIACIGGCIGCAGCICCAGCCCC 33
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                          549 CGATTCTTTGCTACTGGCTGCAGCTGCAGCCCC
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2000US-258952P.
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18-JAN-2001; 2001US-262859P.
16-AUG-2001; 2001EP-0118884.
16-AUG-2001; 2001US-312825P.
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hes 33; Conservative
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                                                                                                                                                                                                                                                                                                   Human CYP3A5
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Length 830; Indels 9

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screened for the presence/absence of a polymorphic variant, preferably at positions -475 or -147 of the DNA of the 5' flanking region adjacent to the CYPAS coding sequence. The variants are present in an activator to the CYPAS coding sequence. The wariants are present in an activator protein-3 (AP-3) motif and/or a basic transcription element (BTE). The polymorphisms caused for the passor of the presence of variants can be used to identify subjects with a high or the presence of variants can be used to identify subjects with a high or low drug metabolizing phenotype associated with cytochrome CYPAS expression. Primers are used which in addition to hybridizing to the site of interest, are capable of introducing a restriction site which is absent in either the wild type sequence or polymorphic variants. Restriction enzyme cleavage analysis can then be used to indicate the presence or absence of the variant. The methods are used to establish, before treatment with a drug, whether the drug will be effectively metabolized by the patient, to identify compounds and transcription factors that can bind to a DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name= "Single nucleotide polymorphism"
//standard_name= "Single nucleotide position -475. Presence
    of a G in variants destroys an AP-3 site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying subjects with a high drug metabolizing phenotype associated with cytochrome CYP3A5 expression for establishing whether a drug will be metabolized by the subject
                                                                                                                                                                                                                                               CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism; Activator protein-3 motif; AP-3; basic transcription element; drug metabolism; phenotype; ss.
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                                                                                                                                                          Cytochrome P450 CYP3A5 gene 5' flanking region (-1343 to +3).
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                                                                               31-OCT-2000 (first entry)
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CYPRAS gene. The invention is useful in an in vitro method for dentifying a polymorphism. The invention is also useful for useful for diagnosing a disorder related to the presence of a molecular variant of a CYPRAS or susceptibility to such a disorder, where the disorder is cancer, or diseases including cardiovascular diseases, diabetes and AIDS. The invention can further be used for the preparation of a diagnostic composition for diagnosing a disease in a subject having a genome composition for diagnosing a disease in a subject having a genome composition for diagnosing of the CYPRAS gene, where the subject is an African American. The molecules of the invention are as forensic markers and in pharmacological studies. The present nucleic acid sequence represents a genomic DNA sequence that contains a region in which a polymorphism of the human CYPRAS gene was detected.
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                                                                                                                                                                                                                                             Human; CYP3A5; polymorphism; cancer; cardlovascular disease; diabetes;
AIDS; African American; forensic marker; pharmacological; cytostatic;
antidiabetic; anti-HIV; gene therapy; ds.
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Pred. No. 0.012;
0; Mismatches 1; Indels 0;
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1164 CGATTCTTTGCTACTGGCTGCAGCTGCAGCCCC 1196
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                                                                                                                                                                                                                Human CYP3A5 gene polymorphic DNA sequence
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16-JAN-2001; 2001EP-0100172.
18-JAN-2001; 2001EP-0100172.
16-ANG-2001; 2001EP-01884.
16-AUG-2001; 2001US-312825P.
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97.0%;
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29-DEC-2000;
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Homo sapiens,

21-OCT-2002

ABK99524;

28-DEC-2000; 29-DEC-2000; 216-JAN-2001; 218-JAN-2001; 2

16-AUG-2001; 16-AUG-2001;

28-DEC-2000;

us-10-085-612-2.rng

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The present invention relates to a new CYP3AS polynucleotide encoding a polypeptide, where the polynucleotide is capable of hybridising to a CYP3AS gene. The invention is useful in an in vitro method for identifying a polymorphism. The invention is also useful for useful for diagnosing a disorder related to the presence of a molecular variant of a CYP3AS or susceptibility to such a disorder, where the disorder is cancer, or diseases including cardiovascular diseases, diabetes and AIDS. The invention can further be used for the preparation of a diagnostic composition for diagnosing a disease in a subject having a genome compersing a variant allele of the CYP3AS gene, where the subject is an African American. The molecules of the invention are as forensic markers
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                                                                                                                                           Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
                                                                                                                                                                                 AIDS; African American; forensic marker; pharmacological; cytostatic; antidiabetic; anti-HIV; gene therapy; ds.
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                                                                       Human CYP3A5 gene polymorphic DNA sequence #13,
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2001EP-0100172
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16-AUG-2001; 2001EP-0118884.
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                                                                                                                                                                                                                                                                                          Homo sapiens.
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21-OCT-2002
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                                                                                                                                                                                                                                                                                                                     Human, CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
AIDS; African American; forensic marker; pharmacological; cytostatic;
antidiabetic; anti-HIV; gene therapy; ds.
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2000US-258684P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-583628/62.
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Matches 32; Conserv
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Indels

ABK99421;

RESULT 13
ABK99421
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Query Match

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Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer, cardiovascular diseases, diabetes and AIDS, and for identifying
                                                                                                                                                                                                                                                                                                     (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                              28-DEC-2000; 2000US-258684P.
29-DEC-2000; 2000US-258952P.
16-JAN-2001; 2001EP-0100172.
18-JAN-2001; 2001US-262859F.
16-AUG-2001; 2001EP-0118884.
                                                                                 21-DEC-2001; 2001WO-EP15290
                                                                                                                                                                                                                                                          16-AUG-2001; 2001US-312825P
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Job time: 265.808 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymorphisms -
W0200253775-A2
                                                                                                                                                                                                                                                                                                                                                Wojnowski L,
                                                                                                                            28-DEC-2000;
                                      11-JUL-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a new CYP3A5 polynucleotide encoding a polymeptide, where the polynucleotide is capable of hybridising to a CYP3A5 gene. The invention is useful in an in vitro method for identifying a polymorphism. The invention is also useful for useful for diagnosing a disorder related to the presence of a molecular variant of a capacity or susceptibility to such a disorder, where the disorder is cancer, or diseases including cardiovascular diseases, diabetes and AIDS. The invention can further be used for the preparation of a diagnostic composition for diagnosing a disease in a subject having a genome comprising a variant allele of the CYP3A5 gene, where the subject is an African American. The molecules of the invention are as forensic markers and in pharmacological studies. The present nucleic acid sequence represents a genomic DNA sequence that contains a region in which a polymorphism of the human CYP3A5 gene was detected.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer, cardiovascular diseases, diabetes and AIDS, and for identifying polymorphisms -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, CYP3A5, polymorphism; cancer; cardiovascular disease; diabetes;
AIDS; African American; forensic marker; pharmacological; cytostatic;
antidiabetic; anti-HIV; gene therapy; ds.
AIDS; African American; forensic marker; pharmacological; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27.6; DB 24; Length 624; Pred. No. 0.34; 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 624 BP; 174 A; 134 C; 149 G; 167 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human CYP3A5 gene polymorphic DNA seguence #12.
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                      antidiabetic; anti-HIV; gene therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                 (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hustert E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Figure 4; 138pp; English.
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2000US-258952P.
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18-JAN-2001; 2001US-262859P.
16-AUG-2001; 2001EP-0118884.
16-AUG-2001; 2001US-312825P.
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Best Local Similarity 88.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haberl M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-583628/62
                                                                                                          WO200253775-A2.
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                                                                 Homo sapiens
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The present invention relates to a new CYP3AS polynucleotide encoding a CYP3AS generate the polynucleotide is capable of hybridising to a CYP3AS gene. The invention is useful in an in vitro method for identifying a polymorphism. The invention is also useful for useful for diagnosing a disorder related to the presence of a molecular variant of a CYP3AS or susceptibility to such a disorder, where the disorder is cancer, or diseases including cardiovascular diseases, diabetes and AIDS. The invention for diagnosing a disease in a subject having a genome composition for diagnosing a disease in a subject having a genome composition for diagnosing a disease in a subject having a genome composition. The molecules of the invention are as forensic markers and in pharmacological studies. The present nucleic acid sequence represents a genomic DNA sequence that contains a region in which a polymorphism of the human CYP3AS gene was detected.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGATTCTTTGCTATTGCTGCTGCAGCTATAGCCCTG 98
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Claim 1; Figure 4; 138pp; English.
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Matches 30; Conserv
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Haberl M,

August 27, 2003, 18:15:45

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Appli Appli Appl

19, Appl 19, Appl 43, Appl 50, Appl 50, Appl 2, Appli

Sequence

Sequence 1 Sequence 1 Sequence S

Title: Perfect score:

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Sequence:

Scoring table:

Searched:

Database

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Sequence 17, Appl
Sequence 1114, Appl
Sequence 1114, Appl
Sequence 66, Appl
Sequence 50, Appl
Sequence 21, Appl
                                                                                                                                   Sequence 2, A Sequence 1, A Sequence 51, A Sequence 51, A
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APPLICANT: Rebix, Carolyn
APPLICANT: Rebix, Carolyn
TITLE OF INVENTION: CYP344 NFSE Variant and Methods of Use Therefor
FITLE OF INVENTION: CYP344 NFSE Variant and Methods of Use Therefor
FILLE PERFENCE: PENN-0655
CURRENT APPLICATION NUMBER: US/09/372,339
CURRENT APPLICATION NUMBER: US/09/372,339
EARLIER APPLICATION NUMBER: 60/096,586
EARLIER PILING DATE: 1998-08-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 2
LENGTH: 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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APPLICANT: Lichter, Jay
APPLICANT: Clichter, Jay
APPLICANT: Clichter, Jay
APPLICANT: Clichter, Jay
APPLICANT: Clichter, Jay
TILE OF INVENTION: GENOTPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR RILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENDIA. 29
                            US-09-177-359-37
US-09-702-705-1114
US-09-36-457-1114
US-09-149-476-66
US-09-149-476-631
US-09-149-476-231
                                                                                                                                 3 US-09-103-840A-1
3 US-09-103-840A-1
10 C-08-949-15-51
US-09-819-964-51
US-08-306-691B-19
PCT-US93-06-691B-19
US-09-144-367-43
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US-08-951-621-50
                                                                                                                                                                                                                                                                                           US-08-688-342-2
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09144367
Patent No. 6432639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-372-339-2; Sequence 2, Application US/09372339; Patent No. 6174684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 GACAAGGGCAGAGAGAG 7
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CRGANISM: Homo sapiens
US-09-372-339-2
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US-09-144-367-13
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Best Local Similarity
Matches 17; Conserv
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880.0
777.8
777.8
76.7
76.7
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Sequence 2, Appl
                                                                                                                     August 27, 2003, 18:02:39; Search time 37.0385 Seconds (without alignments) 214.504 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 3, Ap
Sequence 17, A
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Sequence 28
Sequence 28
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Sequence 3
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/cgr2_6/ptodata/1/ina/5B_COMB.seq:*
/cgr2_6/ptodata/1/ina/6A_COMB.seq:*
/cgr2_6/ptodata/1/ina/6B_COMB.seq:*
/cgr2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgr2_6/ptodata/1/ina/PcTUS_COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-464-167-28
US-09-158-313-28
US-08-154-019-29
US-08-461-333-29
US-08-464-167-29
US-08-464-167-29
US-08-476-798-29
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-09-205-258-131
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US-08-920-422-17
                                                                                                                                                                                                                                                                                                         569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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18
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Score

Result Š.

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Gaps

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Query Match 85.6%; Score 15.4; DB 4; Length 45546; Best Local Similarity 94.1%; Pred. No. 1.4e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0;
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88.9%; Pred. No. 1.4e+02;
Live 0; Mismatches 2; Indels
                                                                         APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Sprinkle, Terry Joe Curtis
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCS103
CURRENT APPLICATION NUMBER: 05/09/146,053A
CURRENT PILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09144367
Patent No. 6432639
GENERAL INFORMATION:
GENERAL INCOMATION:
APPLICANT: Lichter, Jay
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTON: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
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GENERAL INFORMATION:
PAPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
                  Sequence 6, Application US/09146053A Patent No. 6399349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-146-053-6
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CONGANISM: H. sapiens
US-09-144-367-12
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US-09-144-367-12/c
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    JS-09-146-053-6
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LENGTH: 32
                                                                                                                                                                                                                                                                                                  SEQ ID NO 6
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                                       Gaps
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    DB 3; Length 1345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1345;
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                                          Indels
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Sequence 44, Application US/09144367

Patent No. 6432639

GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
ITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4

FILE REPERBENCE: SEQ-129

CURRENT APPLICATION NUMBER: US/09/144,367

CURRENT PILING DATE: 1999-08-31

PRIOR FILING DATE: 1997-09-10

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 44

LENGTH: 19
                                                                                                                                                                                                         Sequence 3, Application US/09144367

Patent No. 6432639

GENERAL INPORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TILLE OF INVERMION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURENY FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 06/058,612
PRIOR PILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE FEASESE for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 4;
Pred. No. 53;
Score 16.4; DB; Pred No. 34; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.4; Di
Pred. No. 70;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    806 GACAAGGGCARGAGAGAG 823
                                                                                                    806 GACAAGGCCAGGAGAGA 823
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                                                                               1 GACAAGGGCAGGACAGAG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.6%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.9%;
88.9%;
Query Match 91.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: H. sapiens
US-09-144-367-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: Other
; LOCATION; (0)...(0)
US-09-144-367-3
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US-09-144-367-3
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Pieper, Frank Krimpenfort, Paul J.A

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E: Townsend and Townsend and Crew One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                             COUNTY:

COUNTY:
COUNTY:
COUNTY:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: IRM PC compatible
COMPUTER: IRM PC COMPATIBLE
COMPUTER: IRM PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1995
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 17-NUV-1990
PRICA DATE: 27-NUV-1990
PRICA DATE: 27-NUV-1990
PRICA DATE: US 07/619,131
FILING DATE: US-DEC-1889
ATTORNEY, AGENT INFORMATION:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1899
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     % Sequence 28 Application US/08464167; Sequence 28 Application US/08464167; Patent No. 6013857; SEMERAL INFORMATION: APPLICANT: Deboer, Herman A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACAAGGGCAGGACAGAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-08-461-333-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.2
Best Local Similarity 88.9
Matches 16, Conservative
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California
                                                                              San Francisco
Californía
       CORRESPONDENCE ADDRESS:
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                                                                                                                                   USA
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APPLICANT
APPLICANT
APPLICANT
                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: 8
STATE:
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APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
TITLE OF INVENTION: Production of Recombinant Polypeptides TITLE OF INVENTION: by Bovine Species and Transgenic Methods NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STARE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.2%; Score 14.8; DB 1; Length 807;
88.9%; Pred. No. 1.9e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,019
FILING DATE: 16-NOV-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lichescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
FELECOMUNICATION INFORMATION:
TELEPROME: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-UN-1993
PRIOR APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-UN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-TUN-1992
RAPA APPLICATION NUMBER: US 07/619,131
PRIOR APPLICATION NUMBER: US 07/619,131
PRIOR APPLICATION NUMBER: US 07/414,745
FILING DATE: 27-NOV-1990
PRIOR APPLICATION NUMBER: US 07/444,745
FILING DATE: US 07/619,131
APPLICATION NUMBER: US 07/444,745
FILING DATE: 10-DEC-1989
ATTORNEY AGENT INFORMATION:
NAME: Tichschart TOOLOGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/08461333;
Patent No. 5741957;
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Platenburg, Gerald
APPLICANT: Platenburg, Gerald
APPLICANT: Pleeper, Frank
APPLICANT: Rimpenfort, Paul J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ||||||| |||| ||||| 411 GACAGGACAGGTCAGAG 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 88.9
Matches 16; Conservative
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US-08-461-333-28/c
                                                                                                                                                                                                             COUNTRY:
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Gaps
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APPLICANT: Heyneker, Rein
APPLICANT: Heyneker, Rein
APPLICANT: Platenburg Gerald
APPLICANT: Lee, Sang He
APPLICANT: Lee, Sang He
APPLICANT: Rimpenfort, Paul J.A.
APPLICANT: Rrimpenfort, Paul J.A.
APPLICANT: Properties Production of Recombinant Polypeptides
TITLE OF INVENTION: DY Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                ö
82.2%; Score 14.8; DB 1; Length 807; 88.9%; Pred. No. 1.9e+02;
                                                                2; Indels
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GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Pieper, Erank
APPLICANT: Preper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: Dy Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.2%; Score 14.8; DB 3; Length 807; Best Local Similarity 88.9%; Pred. No. 1.9e+02; Matches 16; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1:0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-UNN-1995
                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,313
                                                                                                                           CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
PRIOR DATE: 01-DEC-1989
ATGNERY-YGEWN INFORMATION:
NAME: Liebescheutz, Joe 0.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 37,505
REPERSORS/POCKET NUMBER: 37,505
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-476-798-28/c
; Sequence 28, Application US/08476798
; Patent No. 6140552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 GACAAGGACAGGTCAGAG 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 807 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94105
                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-158-313-28
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Sequence 28, Application US/09150313
Fatent No. 6066725
GENERAL INFORMATION:
APPLICANT: Strijker, Rein
APPLICANT: Strijker, Rein
APPLICANT: Flatenburg, Gerald
APPLICANT: Platenburg, Description of Recombinant Polypeptides:
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESSED: Townsend and Townsend and Crew
ADDRESSED: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
STREET: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
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                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRD PC compatible
COMPUTER: IRD PC compatible
COMPUTER: PACTOR PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,167
FILING DATE: 05-UN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                        PILLING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRICE APPLICATION: 800
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
FILING DATE: 15-JUN-1993
PRICE APPLICATION NUMBER: US 07/695,956
PILING DATE: 15-JUN-1992
PRICE APPLICATION NUMBER: US 07/619,131
PRICE APPLICATION NUMBER: US 07/619,131
PRICE APPLICATION NUMBER: US 07/444,745
PRICE APPLICATION NUMBER: US 07/444,745
PRICE APPLICATION NUMBER: US 07/444,745
PRICE DATE: 01-DEC-1989
APPLICATION NUMBER: 37,505
PREFERENCE/DOCKET NUMBER: 16994-003124
TELETRAX: 415-543-5043
INFORMATION TREORMATION:
TELETRAX: 415-543-5043
INFORMATION POR SEQ. DN 00: 28:
SEGURATION POR SEQ. DN 00: 28:
TELETRAX: AND DASE PAILS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 GACAAGGACAGGTCAGAG 394
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GACAAGGGCAGGACAGAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-464-167-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94105
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US-09-158-313-28/c
COUNTRY:
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APPLICANT: Frieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
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MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC COMPATIBLE
SPERATING SYSTEM: PC-FOS_MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTONNEY/AGENT INPORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-543-9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
FILING DATE: 05-JUN-1995
CLASHICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/08461333 Patent No. 5741957 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Deboer, Herman A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 824 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
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APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.2%; Score 14.8; DB 3; Length 807;
88.9%; Pred. No. 1.9e+02;
tive 0; Mismatches 2; Indels
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PRIOR APPLICATION: 000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 15-010-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1980
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe 0.
REGISTRATION NUMBER: 37,505,50310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310,00310
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FILING DATE: 16-NOV-1993
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/077,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISSICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) US-08-476-798-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deboer, Herman A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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STATE: California
COUNTRY: USA
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APPLICANT: Deboer,
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US-08-154-019-29/c
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Pieper, Frank
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.2%; Score 14.8; DB 3; Length 8 88.9%; Pred. No. 1.9e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
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APPLICATION NUMBER: US/09/158,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                               16994-003124
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REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/09158313
Patent No. 6066725
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
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APPLICATION NUMBER: 08/476,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACAAGGGCAGGACAGAG 18
                                                               NAME: Liebescheutz, Joe O. REGISTRATION NUMBER: 37,505
                                                                                                                  REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                          TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     824 base pairs
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Matches 16, Conservative
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US-09-158-313-29/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-464-167-29
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                                                                                                                                                                                                                                                                                                                  LENGTH:
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APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.2%; Score 14.8; DB 1; Length 824;
88.9%; Pred. No. 1.9e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STAME: California COUNTRY: USA
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COMPUTER: IBW PC compatible
OPERATING STSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patcentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,167
FILING DATE: DOJUN-1995
CLASSIFICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joo e o.
REGISTRATION NUMBER: 37,505
REFERRNCE/DOCKET NUMBER: 16994-003123
TELEPHONE: 415-543-5600
TELEPHONE: 415-543-5603
TELEPRAX: 415-543-5603
TELEPRAX: 415-543-5603
TELEPRAX: 415-543-5003
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TELEPRAX: CHASACTERISTICS: CONTRACTION: CONTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/08464167
Patent No. 6013857
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strilker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
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MOLECULE TYPE: DNA (genomic)

US-08-461-333-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.39,
These 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 824 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT:
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δŽ g

Search completed: August 27, 2003, 19:42:01 Job time : 42.0385 secs

417 GACAAGGACAGGTCAGAG 400

Op

Human CYP3A4 gene 5'-flanking region Human secreted pro

Human CYP3A4 gene Oligonucleotide #2 Listeria monocytog

Human kidney amino Human cDNA differe Human immune/haema Secreted protein g Human secreted pro

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/standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytochrome P450; CYP3A4; CYP3A5; glutathione S-transferase;
GSYM1, breast cancer; therapy; chemotherapeutic agent; variant;
drug-drug interaction; drug adverse effect; anti-cancer agent; SNP;
enzyme; single nucleotide polymorphism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytochrome P450 (CYP) 3A4 polymorphic variant DNA fragment.
AAX28296
ABK68745
AAA61269
                                                                                      ABK83564
AAK86612
ABZ74371
                                                                                                                                                                                                                     AAD45762
AAD36217
AAD45776
AAX28305
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ABA68729
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AAK42855
AAI23619
AAI48930
AAI09234
ABS42487
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ABA45639
ABA56143
                                      AAX28287
ABK68748
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ABZ73544
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  26-FEB-2002; 2002WO-US06135
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 WO200268448-A1
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Synthetic.
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variation
                                                                                                                                                                                                                     AAD45760;
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Nucleic acid seque
Saccharopolyspora
DNA sequence of hu
Human voltage-acti
Human Canlon gene
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                                                                                    August 27, 2003, 17:59:19; Search time 140.192 Seconds (without alignments) 346.595 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                  1: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1980.DAT:*
2: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1981.DAT:*
3: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1982.DAT:*
4: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1983.DAT:*
5: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1981.DAT:*
6: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1985.DAT:*
7: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1985.DAT:*
8: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1988.DAT:*
9: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1989.DAT:*
10: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1989.DAT:*
11: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1989.DAT:*
12: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1989.DAT:*
13: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1992.DAT:*
14: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1992.DAT:*
15: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1992.DAT:*
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17: /SIDS1/gcgdata/geneseg/genesegn-embl/Na1992.DAT:*
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/SIDS1/gcgdata/geneseqr/geneseqn-emb1/NA2001B.DAT:*
/SIDS1/gcgdata/geneseqr/geneseqn-emb1/NA2002.DAT:*
/SIDS1/gcgdata/geneseqr/geneseqn-emb1/NA2003.DAT:*
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                         Compugen Ltd
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                                                                                                        Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
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AAD45777
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AAZ57020
ABV75557
ABX77171
ABN83124
ABQ80552
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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18
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91.1 1345
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91.1 172637
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Match Length
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116:
120:
120:
13:
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Score

Result <u>ي</u>

breast cell foetal liver #14158 for g brain expres bone marrow #1352 for g #17616 used #225 used t liver single genome-deriv

Human Probe Human Human Probe Probe Probe Human

ORFX polynuc human polynu human polynu

Human Novel Human

breast cell foetal liver

Human Human

ovarian canc

Human cytochrome P Human CYP3A4 promo Human promoter. -39 PCR primer for Hum Human breast cell

Human secreted pro Secreted protein-e Human secreted pro

Perfect score:

Run on:

scoring table: Sequence:

Searched:

Database

Nucleotide sequenc Nucleotide sequenc Mouse ischaemic co

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The invention relates to a nucleic acid molecule comprising at least one base variation from human cytochrome P450 (CYP) 3A4 or CYP3A5 sequence.

Nucleic acid molecules of the invention are useful for identifying polymorphisms associated with CYP3A4, CYP3A5 or glutathione S-transferase (GST) MI substrates which influence breast cancer treatments. They are also useful in diagnostic purposes to identify individuals having a polymorphic genotype which influence the outcome of breast cancer treatments and the selection of chemotherapeutic agents used to treat breast cancer. The polymorphisms detected are used to screen altered metabolism of CYP3A4, CYP3A5 or GSTM1 substrates, potential drug-drug interactions, drug adverse effects, likelihood of successful clinical outcome following treatment with anti-cancer agents such as cisplatin, cyclophosphanide and/or BCMU. The present sequence is human CYP3A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hall J, Petros WP, Vredenburgh JJ, Colvin OM, Marks JR;
                                                      Colvin OM, Marks JR;
                                                                                                                       New nucleic acid molecule useful for identifying polymorphisms associated with CYP3A4, CYP3A5 or GSTM1 substrates which influence breast cancer treatments, comprises at least one base variation from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytochrome P450; CYP3A4; CYP3A5; glutathione S-transferase;
polymorphism; GSTM1; breast cancer; therapy; chemotherapeutic agent;
drug-drug interaction; drug adverse effect; anti-cancer agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule useful for identifying polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natch 100.0%; Score 18; DB 24; Length 18; Local Similarity 100.0%; Pred. No. 32; les 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human promoter -392 CYP4503A4 specific probe #2.
                                                     Hall J, Petros WP, Vredenburgh JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 7 A; 3 C; 8 G; 0 U; 0 other;
                                                                                                                                                                              human CYP3A4 or CYP3A5 sequence -
                                                                                                                                                                                                              Claim 1; Page 12; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACAAGGGCAGGACAGAG 18
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UYDU-) UNIV DUKE.
                                                                                         WPI; 2002-691652/74.
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(DNAS-) DNA SCI IN
(UYDU-) UNIV DUKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD45777;
                                                     Guida M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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The invention relates to a nucleic acid molecule comprising at least one base variation from human cytochrome P450 (CTP) 3A4 or CTP3A5 sequence. Nucleic acid molecules of the invention are useful for identifying polymorphisms associated with CYP3A4, CYP3A5 or glutathione 5-transferase (GST) MI substrates which influence breast cancer treatments. They are also useful in diagnostic purposes to identify individuals having a polymorphic genotype which influence the outcome of breast cancer treatments and the selection of chemotherapeutic agents used to treat breast cancer. The polymorphisms detected are used to screen altered metabolism of CYP3A4, CYP3A5 or GSTMI substrates, potential drug-drug interactions, drug adverse effects, likelihood of successful clinical outcome following treatment with anti-cancer agents such as cisplatin, excloses the content of the present sequence is human promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a PCR primer for the human CYP3A4 gene promoter. The invention relates to a CYP3A4 sequence polymorphism, which is part of a non-naturally occurring chromosome. Nucleic acids comprising the CYP3A4 polymorphic sequences can be used to screen patients for altered metabolism for CYP3A4 substrates, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism; CYP3A4 substrate; drug-drug interaction identification; toxin exposure; genetic linkage detection; phenotypic variation; promoter; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
associated with CYP3A4, CYP3A5 or GSTM1 substrates which influence breast cancer treatments, comprises at least one base variation from human CYP3A4 or CYP3A5 sequence -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 8 A; 3 C; 11 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer for Human CYP3A4 gene promoter.
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                                                                                                                                            Example 2; Page 26; 41pp; English.
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nes 17; Conservative
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ID AAX28306 standard; DNA; 29
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Matches
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           THE STATE OF THE S
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Gaps

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Gaps

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Indels

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Mismatches

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Conservative

17;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYP3A4, a member of cytochrome P450 supergene family. The CYP3A4 variant CYP3A4, a member of cytochrome P450 supergene family. The CYP3A4 variant is useful for identifying patients with heightened risk of developing or having prostate cancer and at risk for developing treatment-related leukemia upon administration of an epipodophyllotoxin. By identifying the CYP3A4 variant, a more effective anticancer treatment regimen can be selected. The present sequence represents the nucleic cacid sequence of the CYP3A4 variant CYP3A4-V. This variant comprises an A to G transition that alters the 10 basepair nifedipine-specific element located at -287 to -296 base pairs from the transcription start site of CYP3A4.
              result from environmental or occupational exposure to toxins. They can also be used to establish animal, cell culture and in vitro cell-free models for drug metabolism. Polymorphic CVP3A4 gene sequences can be used for expression studies to determine the effect of promoter and/or intron sequence variations on mRNA expression and stability. The polymorphisms are also used as single nucleotide polymorphisms to detect genetic linkage to phenotypic variation in activity and expression of CYP3A4. The nucleic acids can also be used to generate genetically modified non-human animals or site specific gene modifications in cell lines.
  drug-drug interactions, and adverse/side effects as well as diseases that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid sequence encoding a variant of CYP3A4, involved in the metabolism of aflatoxin B1 and drugs, useful for identifying patients with increased risk of developing or having prostate cancer
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYP3A4; cytochrome P450; variant; prostate cancer; leukemia; epipodophyllotoxin; human; anticancer; ds.
                                                                                                                                                                                                                                                       Length 29;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1345 BP; 352 A; 314 C; 357 G; 322 T; 0 other;
                                                                                                                                                                                                                                                     Score 16.4; DB 20;
Pred. No. 1.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid sequence of CYP3A4 variant CYP3A4-V.
                                                                                                                                                                                                                Sequence 29 BP; 3 A; 12 C; 3 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 33; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA257020 standard; DNA; 1345 BP
                                                                                                                                                                                                                                                                                                                                1 GACAAGGGCAGGACAGAG 18
                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                       91.1%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                      24 GACAAGGGCAGGAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                       Local Similarity 94.4 ies 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rebbeck TR, Felix CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-224371/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-FEB-2000
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                                                                                                                                                                                                                                                         Query Match
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Score 16.4; DB 21; Length 1345; Pred. No. 2.2e+02;

91.1%; 94.4%;

Query Match Best Local Similarity

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New butenyl-spinosyn biosynthetic genes, useful for increasing the production of butenyl-spinosyn insecticidal macrolides, or for changing
                                                                                                                                          Butenyl; biosynthetic enzyme; PKS; polyketide synthetase; macrolide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ABP57678, ABP57679, ABP57680, ABP57681, ABP57682, ABP57705, ABP57705, ABP57707.
                                                                                                                        Saccharopolyspora butenyl-spinosyn biosynthetic gene cluster 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waldron C;
                                                                                                                                                                                                                                                                                                                                                                                  /transl_except= (pos:62879..62881,aa:Xaa)
/transl_except= (pos:62939..62941,aa:Xaa)
/note= "Xaa=Uhknown. No start codon given"
complement (65226..66602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gustafson GD,
                                                                                                                                                                                                                                                    note= "No start codon given"
9553..29086
                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "ORF RII"
/note= "No start codon given"
complement (68759..69676)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "No start codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "ORF RIII"
                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bullard BS,
                                                                                                                                                                                                                                                                                                                                                                         'product= "ORF RI"
                                                                ABV75557 standard; DNA; 75236 BP
                                                                                                                                                                                                                                                                                                               "busD"
                                                                                                                                                                                                                   product= "busA"
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                 823
                                                                                                                                                   metabolite; spinosyn; gene; ds.
18
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43945..60639
                                                                                                                                                                                                                                                                                                                                             'product= "bu
52090..63940
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          1 GACAAGGCCAGGACAGAG
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                                                                                                     22-JAN-2003 (first entry)
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                                                                                                                                                                      Saccharopolyspora sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitchell JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2002.
                                                                                    ABV75557;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a transgenic non-human animal which may be used for assessing the behaviour and/or metabolism of a drug in another animal and which expresses a foreign polypeptide associated with drug behaviour and/or metabolism. The invention also comprises a nucleic construct for use in producing the above transgenic non-human animal and an animal of interest, comprising and/or behavior of a drug in transgenic animal and conducting analytical tests to determine drug metabolism and/or behaviour. The transgenic animal is studying drug metabolism and/or behaviour in other animals. The nucleic acid drug metabolism and/or behaviour in other animals. The nucleic acid construct is useful in producing the above transgenic animal and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; transgenic; drug metabolism; behaviour; gene; mouse; pharmacokinetic assay; planmacodynamic assay; toxicology; serum albumin; alpha-acidic glycoprotein; CYP; multidrug resistance protein; MRP; uridine diphosphoglucuronosyl, transferase; UGT; cytochrome P450.
                                                                                                                     that encodes a butenyl-spinosyn biosynthetic enzyme, a butenyl-spinosyn PKS (Polyketide synthetase) domain, or a spinosyn PKS module. The butenyl-spinosyn biosynthetic genes are useful for increasing the production of butenyl-spinosyn insecticidal macrolides. The genes also useful for changing the metabolites or products produced by spinosyn-producing microcapanisms. The present sequence represents a DNA molecule encoding butenyl-spinosyn biosynthetic enzymes.
                                                                                                  The invention relates to a novel DNA molecule comprising a DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New transgenic non-human animal expressing a foreign polypeptide associated with drug behavior and/or metabolism, useful for studying the behavior and/or metabolism of a drug in other animals -
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                   Score 16.4; DB.25; Length 75236;
Pred. No. 2.7e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                Sequence 75236 BP; 10935 A; 21693 C; 28185 G; 14421 T; 2 other;
metabolites or products produced by spinosyn-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence of human BAC clone RP11-757A13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2A; Page 229-295; 408pp; English.
                                                            Claim 2; Page 57-99; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          ABX77171 standard; DNA; 123785 BP
                                                                                                                                                                                                                                                                                                                                                                                                   1 GACAAGGGCAGGACAGAG 18
                                                                                                                                                                                                                                                                                                                   Query Match 91.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2001; 2001AU-0004467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENE STREAM PTY LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2002; 2002WO-AU00485.
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                    microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX77171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; transporter protein; voltage-activated ion channel; gene therapy;
methods are used for producing, breeding and using transgenic animals for pharmacological (e.g. pharmacokinetic or pharmacokine assays) and/or toxicological studies. Nucleic acid sequences used within the invention are serum albumin; alpha-acidic glycoprotein; cytochrome P450 (CPP); uridine diphosphoglucuronosyl transferase (UGP); multidrug resistance proteins and (MRP's). The present sequence represents and consider a transgenic animal within the scope of the
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "Single nucleotide polymorphism"
6762..6944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard_name="Single nucleotide polymorphism" replace (2514..2515,ATC/ACC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Single nucleotide polymorphism"
                                                                                                                                                                                                    Sequence 123785 BP; 34793 A; 24793 C; 26537 G; 37655 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                   Length 123785;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'standard_name= "Single nucleotide polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human voltage-activated ion channel transporter protein gene.
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                            Score 16.4; DB 25;
Pred. No. 2.7e+02;
0; Mismatches 1;
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/*tag d /
/product= "Transporter protein"
/note= "Contains 11 introns"
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/*tag= h
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replace (1546,G)
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                                                                                                                                                                                                                                                                                                                                       1 GACAAGGCAGGACAGAG 18
                                                                                                                                                                                                                                              Query Match 91.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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3108..6761
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3000..3107
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                                                                                                                                                              invention.
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/number= 2

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variation	<pre>/standard_name= "Single nucleotide polymorphism" /*tan_ n</pre>		variation	replace (30 /*tag= al
variation	/.tdg-m.//.tandard.name- "Single nuclectide polymorphism" replace (9044,C)	FT val	variation	replace (31 /*tag= am
variation	/~Lay= 0 //Standard_name= "Single nucleotide polymorphism" replace (9990,A) /*tan= n		variation	replace (31 /*tag= an /*standard n
variation	/standard_name= "Single nucleotide polymorphism" /*tplace (10712,T)		variation	replace (35 /*tag= ao
variation	/standard_name= "Single nucleotide polymorphism" (1855,C)		variation	replace (35 /*tag= ap
variation	/ Lay= 1 / Standard_name= "Single nucleotide polymorphism" replace (12177,6) /*tage 6	7 TT TT T	variation	/standard_r replace (47 /*tag= ag
variation	/standard_name= "Single nucleotide polymorphism"		variation	replace (47 /*tag= ar
variation	/standard_name= "Single nucleotide polymorphism" /*teplace (13406, A)		variation	replace (57 /*tag= as
variation	/-Lay= a /standard_name= "Single nucleotide polymorphism" replace [16751,C) /*tag= v	FT Va	variation	replace (57) /*tag= at /standard r
variation	/standard_name= "Single nucleotide polymorphism" replace (20631,G) /*fac	FT ex	exon	56497566 /*tag= au /number= 6
variation	/standard_name= "Single nucleotide polymorphism" replace (20587,G) /**ar	FT FT FT	intron	566521096 /*tag= av
variation	/standard_name= "Single nucleotide polymorphism" replace (20793,A)	FT va FT.	variation	replace (56 /*tag= aw
varíation	/standard_name= "Single nucleotide polymorphism" replace (20935,G)	FT VA	variation	replace (60
exon	/cus-z-z-z-z-z-z-z-z-z-z-z-z-z-z-z-z-z-z-z	FI FI FI	variation	replace (60
intron		FT VA	variation	replace (6)
exon	/number= ab 2504825187	FT va	variation	/standard_replace (70 /*tag= ba
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exon	2527625404 /*tag= ae /*tag= ae	FF		/*tag= bc /standard_
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_name= "Single nucleotide polymorphism" 73818, G) _name= "Single nucleotide polymorphism" 30649,G) _name= "Single nucleotide polymorphism" [5397,T] _name= "Single nucleotide polymorphism" _name= "Single nucleotide polymorphism" 73323,G) _name= "Single nucleotide polymorphism" [3438.A] _name= "Single nucleotide polymorphism" 14035,C) _name= "Single nucleotide polymorphism" 74832,C) _name= "Single nucleotide polymorphism" 35034,A) "name= "Single nucleotide polymorphism" 17264,C) _name= "Single nucléotide polymorphism" 551 _name= "Single nucleotide polymorphism" 60645,T) _name= "Single nucleotide polymorphism" 60709,A) _name= "Single nucleotide polymorphism" 67297,T) _name= "Single nucleotide polymorphism" 10472,1) _name= "Single nucleotide polymorphism" \$1479,G) name= "Single nucleotide polymorphism"
17020,1) _name= "Single nucleotide polymorphism" (0899,G) _name= "Single nucleotide polymorphism" [2558,G] _name= "Single nucleotide polymorphism" 31835,A) _name= "Single nucleotide polymorphism" 35183,G) 56912, G) 9657

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/number= 15
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                                                                                                                                                          Human; CanIon; neuroleptic; hypotensive; anticonvulsant; analgesic; antiarrhythmic; antianginal; cardiant; antimanic; antidepressant; gene therapy; schizophrenia; voltage-gated ion channel; bipolar disorder; central nervous system disorder; cardiovascular disorder; hypertension; pain; epilepsy; chromosome 13q; gene; ds.
                                           Gaps
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106567..106758
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/note= "Biallelic marker: 99-79314-201/Al0"
100509
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fnote= "Biallelic marker: 99-79336-369/A8"
77568..77699
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98226..98393
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hote= "Biallelic marker: 99-79335-60/A7"
2093..52179
                                          Indels
                            Score 16.4; DB 24;
Pred. No. 2.7e+02;
0; Mismatches 1;
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43726..43868
                                                               ABQ80552 standard; DNA; 237961 BP
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/number= 14
159797..159868
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                                                                                                                                              Human Canlon gene fragment #2.
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43998..44102
/*tag= b
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/number= 10
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94.4%;
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/number= 11
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       variation
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The present sequence is a gene fragment for human Canlon, a novel schizophrenia-related voltage-gated ion channel protein. Canlon and its coding sequence are useful in the treatment of schizophrenia, bipolar disorder, or other central nervous system (CNS) conditions, as well as other conditions such as heart conditions and hypertension. Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel schizophrenia-related voltage-gated ion channel polypeptide and dynucleotide useful for identifying modulators and for diagnosing, treating schizophrenia, bipolar disorder or central nervous system disorders
/*tag= o
/note= "Biallelic marker: 99-79322-224/Al3"
166336
                                                        *tag= p
note= "Biallelic marker: 99-79322-473/Al4"
.91292..191428
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/note= "Biallelic marker: 99-79306-182/Al5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 183-246; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simon A,
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231289.231345
/*tag= y
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231589.231709
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/number= 17
211540..211613
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/number= 20
228450..228541
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/number= 24
231813..231944
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/number= 25
232900..233067
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92967..193108
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128630..228752
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25006..225107
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25544..225613
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235355..235459
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Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP;

30-AUG-2000; 2000GB-0021286. 30-AUG-2001; 2001WO-IB01580

WO200218641-A2. Homo sapiens.

CYP3A4; ds.

07-MAR-2002

(GEMI-) GEMINI GENOMICS PLC

5'-flanking region of human CYP3A4 gene.

02-JUL-2002 (first entry)

ABK68745;

806 GACAAGGGCARGAGAGA 823

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1 GACAAGGCCAGGACAGAG 18

ABK68745 standard; DNA; 1345 BP

RESULT 10 ABK68745

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This sequence represents the human CYP3A4 gene promoter.
The invention relates to a CYP3A4 sequence polymorphism,
which is part of a non-naturally occurring chromosome. Nucleic acids
comprising the CYP3A4 polymorphic sequences can be used to screen
patients for altered metabolism for CYP3A4 substrates, potential
drug-drug interactions, and adverse/side effects as well as diseases that
result from environmental or occupational exposure to toxins. They can
also be used to establish animal, cell culture and in vitro cell-free
models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used
for expression studies to determine the effect of promoter and/or intron
sequence variations on mRNA expression and stability. The polymorphisms
are also used as single nuclectide polymorphisms to detect genetic
linkage to phenotypic variation in activity and expression of CYP3A4. The
nucleic acids can also be used to generate genetically modified non-human
and an also be used to generate genetically modified non-human
and also be used to see to
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                       conditions, preferably schizophrenia or bipolar disorder, and also including pain disorders, epilepsy and various cardiovascular disorders such as heart arrhythmias, angina and hypertension. The Canlon gene is located on chromosome 13q. The present sequence comprises a genomic sequence of Canlon, comprising exons 8 to 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism; CYP3A4 substrate; drug-drug interaction identification; toxin exposure; genetic linkage detection; phenotypic variation; promoter; ss.
that block Canlon channels are useful to treat a number of diseases or
                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                             Sequence 237961 BP; 74252 A; 43806 C; 46176 G; 72420 T; 1307 other;
                                                                                                                                                                                                                             y Match
Local Similarity 94.4%; Pred. No. 2.8e+02;
hes 17; Conservative 0; Mismatches 1. 7.201.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated CYP3A4 polymorphic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 29; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   29559 GACAAGGGCAGGGCAGAG 29576
                                                                                                                                                                                                                                                                                                                                                                        1 GACAAGGCAGGACAGAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX28296 standard; DNA; 1345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CYP3A4 gene promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guida M, Lichter JB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and sequence determination oligonuclectides for detecting single nucleotide polymorphisms (SNPs) in the 5'-flanking regions of human exposition 451 of a defined 1345 base pair sequence for CYP2A4 or position 451, 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2A9. The RR primers are useful for amplifying the CYP sequences and the oligonucleotides are useful for amplifying SNPs in the 5'-flanking regions of the CYP3A4 or CYP2C9 genes. The present sequence represents the 5'-flanking regions of the CYP3A4 or CYP2C9 genes. The
                                                                                                                                                                                                                                                                                                                                                                     Novel primer pairs and sequence determination oligonucleotides useful for amplifying and detecting novel single nucleotide polymorphisms in the 5'-flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to PCR primer pairs for amplifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.9%; Score 16; DB 24; Length 1345; 88.9%; Pred. No. 3.4e+02; tive 1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1345 BP; 352 A; 313 C; 356 G; 322 T; 2 other;
                                                                                                                                                                                                                                                                                                                Risinger C, Andersson MK, Lewander T, Olaisson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA61269 standard; DNA; 3881 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACAAGGCCAGGACAGAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1; 47pp; English.
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Best Local Similarity.
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   respectively
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ID AAA612
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AC AAA612
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DT 18-OCT
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Gaps

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Query Match 88.9%; Score 16; DB 20; Length 1345; Best Local Similarity 88.9%; Pred. No. 3.4e+02; Matches 16; Conservative 1; Mismatches 1; Indels

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number and the clone it was derived from are given in the descriptor line.

The invention relates to 31 novel genes and their fragments (nucleic acid sequences: AAA61260-A61293; amino acid sequences AAB12301-B12371) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the amount of the new polypeptides in a pyrucleotides, based on which tissues they are most highly expressed in nolude products for the diagnosis or treatment of cancer, tumours, and include products for the diagnosis or treatment of cancer, tumours, bacterial and fungal infection. The genes are used to generate fusion continues by linking to the gene a human immunoglobulin portion (AAA61251) for increasing stability of the fused protein as compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism; CYP3A4 substrate; drug-drug interaction identification; toxin exposure; genetic linkage detection; phenotypic variation; ss.
                                                                                                                                                                                                                                                                                            Novel human secreted proteins useful for diagnosing, preventing, treating and ameliorating a medical condition e.g. cardiovascular
                      Human; secreted protein; fusion protein; gene therapy;
protein therapy; diagnosis; tissue; cancer; tumour; AIDS;
autoimmune disorder; allergy; cardiovascular; viral; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                  Florence KA, Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 21; Length 3881;
Pred. No. 3.6e+02;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3881 BP; 1043 A; 610 C; 716 G; 1512 T; 0 other;
Human secreted protein gene 10 clone HDPGP94.
                                                             fungal infection; immunosuppressive; ds
                                                                                                                                                                                                                                  Ruben SM, Rosen CA, Ebner R, SE, Carter KC, Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                              laim 1; Page 233-234; 295pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.9%; Scc...
100.0%; Pre/
0; }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX28287 standard; DNA; 19 BP.
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                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                           99WO-US26409.
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Matches 16; Conservative
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                                                                                                            WO200029422-A1.
                                                                                     Homo sapiens.
                                                                                                                                                           09-NOV-1999;
                                                                                                                                                                                   12-NOV-1998;
                                                                                                                                   25-MAY-2000.
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This sequence represents a CYP3A4 sequence polymorphism of the invention, which is part of a non-naturally occurring chromosome. Nucleic acids comprising the CYP3A4 polymorphic sequences can be used to screen patients for altered metabolism for CYP3A4 substrates, potential drug-drug interactions, and adverse/side effects as well as diseases that result from environmental or occupational exposure to toxins. They can also be used to establish animal, cell culture and in vitro cell-free models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used for expression studies to determine the effect of promoters and/or intron sequence variations on mRNA expression and stability. The polymorphisms are also used as single nucleotide polymorphisms to detect genetic linkage to phenotypic variation in activity and expression of CYP3A4. The nucleic acids can also be used to generate genetically modified non-human animals or site specific gene modifications in cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.4; DB 20;
Pred. No. 5.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 7 A; 3 C; 9 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated CYP3A4 polymorphic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 35; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2001; 2001WO-IB01580.
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                                                                                                                        98WO-US18158
                                                                                                                                                                                    97US-0058612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK68748 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.1%
                                                                                                                                                                                                                                                (AXYS-) AXYS PHARM INC.
                                                                                                                                                                                                                                                                                                         Guida M, Lichter JB;
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-215070/18.
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                                                                                                                                                                                 10-SEP-1997;
                                                                                                                        02-SEP-1998;
WO9913106-A1
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                                                            18-MAR-1999
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used to screen for compounds that modulate gene expression, replication

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                                                                                                                                                                                                                                                                                                                    The present invention relates to PCR primer pairs for amplifying and sequence determination oligonucleotides for detecting single nucleotide polymorphisms (SNPS) in the 5'-flanking regions of human eytochrome p450 (OYP) genes encoding CYP3A4 or CYP2A9. The SNPS correspond to position 461 of a defined 1345 base pair sequence for CYP2A9 and PS7, 1049, 1164, 1164, 1556, 1661 and 162 of a 4348 base pair sequence for CYP2A9. The PCR primers are useful for amplifying the CYP sequences and the oligonucleotides are useful for detecting
                                                                       Novel primer pairs and sequence determination oligonucleotides useful for amplifying and detecting novel single nucleotide polymorphisms in the 5' flanking regions of cytochrome p450 (CYF)3A4 and CYP2C9 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNPs in the 5'-flanking regions of the CYP3A4 or CYP2C9 genes. ABK68747-ABK68750 represent previously published oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.6%; Score 15.4; DB 24; Length 19; 94.1%; Pred. No. 5.3e+02; Live 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for detecting a polymorphism in the CYP3A4 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 7 A; 3 C; 9 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes 4b specific contig55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 22; SEQ ID 3941; 180pp; French.
                                                                                                                                                                                                                                                            Disclosure; Page 3; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ71128 standard; DNA; 677 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAAGGCAGGAGAGAG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2002 (first entry)
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nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INSP ) INST PASTEUR.
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WPI; 2002-351712/38
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                                                                                                                                                                                    respectively
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This invention describes the isolation of a novel human aminopeptidase P (AmP). This protein is used to produce recombinant AmP and can be used for gene therapy for treating AmP-deficiency conditions. Its fragments are used as primers and probes to identify patients with homozygous and heterozygous AmP deficiency, including prenatal diagnosis (patients defective in AmP are at risk of developing angiodema if treated with angiotensin-converting enzyme inhibitors), also as antisense inhibitors in cases of excessive AmP expression. The product of the invention is also used to identify AmP-expression. The product of the invention is also used to identify AmP-expression sequences in other animals and to generate transgenic animals, and comparisons of genomic sequences are used to detect mutations. AmP inhibitors are potentially useful as antihypertensive agents and to prevent or treat arterial (re)stenosis antihypertasis. The structure of AmP is used to design synthetic substrates, e.g. for use in AmP assays. AmP, which hydrolyzes N-terminal imple bonds, can be used to degrade industrial protein feeds to free formulations used to treat malabsorption syndrome and for studying its biological role. Antibodies against AmP are used in immunohistochemical methods to study AmP distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prenatal diagnosis; angioedema; antihypertensive agent; atherosclerosis; arterial stenosis; industrial protein feed; malabsorption syndrome; proteinaceous waste degradation; additive; immunohistochemistry; ss.
and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aminopeptidase; human; AmP; gene therapy; treatment; AmP-deficiency;
                                                                            anti-Listeria vaccines.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                          .,0
                                                                                                                                                                                             directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                              Score 15.4; DB 24; Length 677; Pred. No. 6.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                         Sequence 677 BP; 145 A; 133 C; 206 G; 193 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX23520 standard; DNA; 45546 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ACAAGGGCAGGACAGAG 18
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94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
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Sequence 45546 BP; 12027 A; 11359 C; 11380 G; 10780 T; 0 other; XX SO

0; Gaps Query Match 85.6%; Score 15.4; DB 20; Length 45546; Best Local Similarity 94.1%; Pred. No. 7.6e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0;

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Search completed: August 27, 2003, 18:15:44 Job time: 142.192 secs

Sequence 2637, Requence 18, App Sequence 1, Ap

Sequence 1, Sequence 136

Sequence 8
Sequence 8
Sequence 8
Sequence 5

Seguence 41, Appl Seguence 10004, A Seguence 14839, A Seguence 14525, A

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GENERAL INCORMATION:
APPLICANT: Rebbeck, Timothy
APPLICANT: Rebbeck, Timothy
TILLGANT: RELIX, CAROLYN
FILE REFERENCE: PENN-0695
CURRENT APPLICATION NUMBER: US/09/372,339
CURRENT FILE REFERENCE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/96,586
EARLIER PILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09372339
Patent No. 6174684
GENERAL INFORMATION:
TEMERAL INFORMATION:
APPLICANT: Rebbeck, Timothy
APPLICANT: Rebbeck, Timothy
APPLICANT: Relix, Carolyn
FILE REFERENCE: PENN-069
CURRENT APPLICATION WUMBER: US/09/372,339
CURRENT FILING DATE: 1999-08-11
FEALLIER APPLICATION NUMBER: 60/096,586
ERALIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.1%; Score 22.8; DB 3; Length 1345; 92.3%; Pred, No. 4.2; 2; Indels 0
                                                                                                                                                                US-09-252-991A-10004
US-09-252-991A-14839
US-09-252-991A-14525
US-09-397-767-162
US-09-328-352-2637
US-09-450-790A-18
US-08-157-185-1
US-08-157-185-1
US-08-450-797-1
US-09-450-797-1
US-09-450-790A-1
                                                                                     US-09-332-837-1
US-09-016-434-1362
                                                                                                                                                        US-09-620-312D-41
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US-08-428-243-8
                                                                                                                                  PCT-US93-10301-8
                                                                                                                                           US-09-693-147-5
                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1035 TGCTACTGGCTGCAGCTCCAGCCCTG 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 TGCTACTGGCTGCTGCTGCCCCCG 34
                                                                                                                                                                                                                                                                           Sequence 1, Application US/09372339 Patent No. 6174684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 92.3
Matches 24; Conservative
  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-2
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
  US-09-372-339-2
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Sequence 2795, Ap
Sequence 35, Appl
Sequence 3, Appli
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                                                                            August 27, 2003, 18:02:39; Search time 69.9615 Seconds (without alignments) 214.504 Million cell updates/sec
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Sequence 2, Al
Sequence 19,
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Sequence 3, 7
Sequence 3, 7
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Sequence 32,
Sequence 20,
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Sequence 2,
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Sequence 1,
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Sequence 3
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                             1 cgattctttgctactggctgcagctgcagcccg 34
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US-08-294-143-3
US-09-256-331-3
US-09-593-483-3
US-09-545-481-3
US-09-313-2944-2795
US-09-313-2944-2795
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US-08-964-268-20
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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US-07-903-466-32
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US-07-903-466-2
PCT-US93-05794-2
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US-09-257-894-12
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US-08-402-066-3
US-08-402-068-3
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US-09-256-331-1
                                                                                                                                                                                                  569978 seqs, 220691566 residues
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                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                      US-10-085-612-2
34
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                                                                                                                                                                    Scoring table:
                                                                                                                                    Perfect score:
                                                          OM nucleic
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                                                          including application described below:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: NAHUM SONENBERG
APPLICANT: ARNIM PAUSE
APPLICANT: JOB B. HARFORD
APPLICANT: JOB B. HARFORD
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including appli
PRIOR APPLICATION DATA: described below
ATTORNEY/AGENT INFORMATION:
NAME: Walder, 32,327
RESISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (37) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 CTTTGCTACTGGCTGCAGCTGCAGCCCC 33
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COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/294,143
FILING DATE: AUGUST 22, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
RELECOMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09256331
Patent No. 6111077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-256-331-1/c
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                                                                  DB 3; Length 1345;
                                                                                                             2;
                                                                                                                                                                                                                                                                                                                 Sequence 3. Application US/09144367

Patent No. 6432639

GENERAL INFORMATION:
APPLICANT: Lichter, Marco
TITLE OF INVENTION:
FILE REFERENCE: SEQ-12P
CURRENT PILING DATE: 1998-08-31

PRIOR APPLICATION NUMBER: US/09/144,367

CURRENT PILING DATE: 1998-08-31

PRIOR APPLICATION NUMBER: 60/058,612

PRIOR APPLICATION NUMBER: 60/058,612

PRIOR FILING DATE: 1997-09-10

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGESULF 4
US-08-294-143-1/C
Sequence 1, Application US/08294143
SEQUENCE 1, APPLICANT: APPLICANT: APPLICANT: APPLICANT: APRIME PAUSE
APPLICANT: VINCENT J. MILES
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREFT: LYON A T.
                                                             Query Match 67.1%; Score 22.8; Di
Best Local Similarity 92.3%; Pred. No. 4.2;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREEL CALIFORNIA
COUNTRY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 31.D iskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1035 TGCTACTGGCTGCAGCTCCAGCCCTG 1060
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FILING DATE: August 22, 1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: AU CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3
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                                                                                                                                                                                                                                                                                                                                                                                              ZUE: 9007

ZUE: 9007

COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
NEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294.143
FILING DATE: August 22, 1994
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
ATTORNET/AEBMR INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
                                         PATENT NO. 587431
GENERAL INFORMATION:
APPLICANT: NAHUM SONENBERG
APPLICANT: ARNIM PAGSE
APPLICANT: JOE B. HARFORD
APPLICANT: VINCENT J. MILES
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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APPLICANT: VINCENT J. WILLES
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 202/060
TELECOMMUTICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: (5731) 489-1600
TELERA: (673510
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Guite 4700
CITY: Los Angeles
STATE: California
CONTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: Lyon & Lyon
633 West Fifth Street
                         Sequence 3, Application US/08294143
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; Sequence 3, Application US/09256331
; Patent No. 6111077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.1%;
Matches 23; Conservative C
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APPLICANT: NAHUM SONENBERG
APPLICANT: ARNIM PAUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSE: Lyon & Ly
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US-08-294-143-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-294-143-3
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                                                                                       58.8%; Score 20; DB 3; Length 357; diarity 82.1%; Pred. No. 41; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
CORRENT SYSTEM: IBM P.C. DOS 5.0
SOFWARE: WOR'D PATFACT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/593,483
FILING DATE: 14-Jun-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NARUM COMMARIAN PAGES
JOE B. HAREORD
VINCENT J. MILES
TITLE OF INVENTION: METHODS FOR TREATING
HORMONE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION: COLKHOWILY
PRIOR APPLICATION NUMBER: 08/294,143
FILING DATE: CURROWN
ATTONRY/SERVINES CURROWN
NAME: WALDERY RICHARD
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZDF: 90071
COMPUTER FADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 CTITGCTACTGGCTGCAGCTGCAGCCCC 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 cridecercieciecieciecieciec
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Sequent No. 6410715
GENERAL INFORMATION:
APPLICANT: NAHUM SONENBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.19
Matches 23; Conservative
  ; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-256-331-1
                                                                                                          Best Local Similarity
Matches 23; Conserv
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                                                                                            Query Match
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APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOFIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 2795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chiang, Christina H.
APPLICANT: Chiang, Christina H.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: No. 6451319e1 Recombinant And Mutant Adenoviruses
FILE REPRENCE: $70993K US
CURRENT APPLICATION NUMBER: US/09/545,481
CURRENT PELING DATE: 2000-04-07
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN OF: 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.8%; Score 20; DB 4; Length 829; Best Local Similarity 82.1%; Pred. No. 48; Matches 23; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 56.5%; Score 19.2; DB 4; Best Local Similarity 75.0%; Pred. No. 1.8e+02; Matches 24; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12572 GATTATTTTCACAGGCTGCCGCTGTAGCCCC 12603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GATICITIGCIACTGGCIGCAGCIGCAGCCCC 33
APPLICATION NUMBER: 08/294,143
FILING DATE: CUNROWN>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERBENGENCYET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:
TELEPRONE: (213) 489-1600
TELERA: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 CTTGGGGTCTGGCTGCTGCTGCCCC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CTTTGCTACTGGCTGCAGCTGCAGCCCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2795, Application US/09313294A Patent No. 6476212 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
; ORGANISM: Bovine adenovirus type 1
US-09-545-481-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-545-481-3; Sequence 3, Application US/09545481; Patent No. 6451319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOE B. HARFORD
VINCENT J. MILES
TITLE OF INVENTION: METHODS FOR TREATING
HORMONE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
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APPLICATION NUMBER: US/09/593,483
FILING DATE: 14-Un-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 CTTTGCTACTGGCTGCAGCTGCAGCCCC 33
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/294,143
FILING DATE: HAGUST 22, 1994
ATTORNET/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
RESTSENCE/COKET NUMBER: 32,327
RELECHONE (131) 489-1600
TELECHONE (131) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREFT: 633 West Fifth Street
Suite 4700
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/256,331 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09593483; Patent No. 6410T15; GENERAL INFORMATION: APPLICANT: NAHUM SONENBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     storage
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                 Los Angeles
California
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                                                                      U.S.A.
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                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-256-331-3
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Op δ

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GENERAL INPONATION:
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
ITILE OF INVENTION: ANTIENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSIO
FILE REFERENCE: RTS-0279
CURRENT APPLICATION NUMBER: US/09/907,843
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 3.
                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.6e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                   Query Match 55.9%; Score 19; DB 3; Length 4550; Best Local Similarity 81.5%; Pred. No. 1.5e+02; Matches 22; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mannane, John P.
APPLICANT: Mannane, John P.
APPLICANT: Mannane, John P.
APPLICANT: Rapp, Leon N.
APPLICANT: Tu, Loh C.
TITLE OF INVENTION: Gene for Ataxia-Telangiectasia
TITLE OF INVENTION: Complmentation Group D (AIDC)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., one Market
STREET: Plaza
                 NAME/KEY: misc_feature
| LOCATION: (2920)
| COTHER INFORMATION: n represents a, c, t or g. |
| FEATURE: nisc_feature |
| LOCATION: (3069) |
| GCATION: (3069) |
| GC-09-103-663-35
                                                                                                                                                                                                                                                                                                                                                                 1872 ATTCTTAGATAGTGGCTGGAGCTGTAG 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 TCCTTTGGTGGTGGCTGCAGCGCAGC 409
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                                                                                                                                                                                                                                                                                                                                      3 ATTCTTTGCTACTGGCTGCAGCTGCAG 29
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/07903466 Patent No. 5395767 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-907-843-3
; Sequence 3, Application US/09907843
; Patent No. 6440739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.9%;
Best Local Similarity 81.5%;
Matches 22; Conservative C
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STATE: California
COUNTRY: San Francisco
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (572)...(4348)
US-09-907-843-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-07-903-466-32/c
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APPLICANT: Kinet et al.

TITLE OF INVENTION: Isolation, characterization, and use of the human beta TITLE OF INVENTION: Isolation, characterization, and use of the human beta TITLE OF INVENTION: immunoglobulin E.

TITLE OF INVENTION: immunoglobulin E.

FILE REFERENCE: 50490

CURRENT APPLICATION NUMBER: US/09/103,663D

CURRENT APPLICATION NUMBER: US/09/103,663D

CURRENT FILING DATE: 1998-06-23

EARLIER PAPILIOATION NUMBER: 07/869,933

EARLIER FILING DATE: 1992-04-16

NUMBER OF SEQ ID NOS: 35

OSCIPHARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                         Length 286;
                                                                  FEATURE:
// NAME/KEX: misc_feature
// OTHER INFORMATION: Incyte ID No. 6476212 700553275H1
US-09-313-294A-2795
                                                                                                                                                                                    Query Match 55.9%; Score 19; DB 4; Best Local Similarity 81.5%; Pred. No. 97; Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (2633)
OTHER INFORMATION: n represents a, c, t or g.
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OTHER INFORMATION: n represents a , C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 35, Application US/09103663D
; Patent No. 6171803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n represents a,
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NAME/KET: misc_feature
LOCATION: (2549)..(2552)
OTHER INFORMATION: n represents a,
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NAME/KEY: misc_feature
LOCATION: (2612)..(2614)
OTHER INFORMATION: n represents a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n represents a,
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NAME/KEY: misc_feature
LOCATION: (2526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (735)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1362)
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LOCATION: (2517)
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LOCATION: (578)
                      TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-103-663-35/c
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LENGTH: 4550
LENGTH: 286
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Sequence 32, Application PC/TUS9305794

Sequence 32, Application PC/TUS9305794

GENERAL INFORMATION:

TITLE OF INVENTION: Gene for Ataxia-Palanqiectasia

TITLE OF INVENTION: Gene for Ataxia-Palanqiectasia

TITLE OF INVENTION: Gene for Ataxia-Palanqiectasia

TITLE OF INVENTION: Complementation Group D (ArDC)

NUMBESSER: Leona L. Lauder

STREET: 177 Post Street, Suite 800

CITY: San Francisco

STREET: 177 Post Street, Suite 800

CITY: San Francisco

STREET: 2177 Post Street, Suite 800

CITY: San Francisco

STREET: 177 Post Street, Suite 800

CITY: San Francisco

STREET: 177 Post Street, Suite 800

CITY: San Francisco

STREET: 177 Post Street, Suite 800

COMPUTR: Pan Francisco

STREET: 241084731

COMPUTR: Patentin Release #1.0, Version #1.25

CURRENA APPLICATION NUMBER: PCT/US93/05794

FILING DATE: 19930618

FILING DATE: SAUGHENCE TOWN SEQ. 100 NO: 32: SEQUENCE CHARACTER TELECOMMUNICATION FOR SEQ. 10 NO: 32: LEBNORH: 1.5-421-453

INFORMATION FOR SEQ. 10 NO: 32: LEBNORH: 1.5-421-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.3%; Score 18.8; DB 1; Length 238; Best Local Similarity 76.7%; Pred. No. 1.1e+02; Matches 23; Conservative 0; Mismatches 7; Indels
  Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 CGACCCGTTGCTCCTGGAGGCATCTGCAGC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGATTCTTTGCTACTGGCTGCAGC 30
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                     LENGTH: 238 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 238 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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MOLECULE TYPE: I
HYPOTHETICAL: NO
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Search completed: August 27, 2003, 19:42:02 Job time : 70.9615 secs

CC011462 PUDG231TD
AA63867 LD18261.5
BH613513 SALK.0343
BH214265 SALK.0343
BH214265 SALK.0343
BH214265 SALK.0343
BH214265 SALK.0104
A432574 A4735574
BL730257 G01563625
BJ219877 BJ219877
AL288196 Tetraodon
BUS59835 AGENCOURT
BM472533 AGENCOURT
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BM67182 TGTACOORT
BM6718194 TETRAOGON
BM67581 170006874
BM578815 170006874
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BM578815 UT-HF-BP0
BX58840 LH-BP0
BX58840 LH-BP0
BX58840 LH-BP0
BX58840 LHC40609.X
BF88163161.X

Searched:

Database

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Result

Sednence:

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Title:

Run on:

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BZ571326 802 bp DNA linear GSS 17-DEC-2002 msh2_1835.x1 msh Pseudomonas aeruginosa genomic clone msh2_1835,
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Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M., Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
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Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
CC011462
AAS38677
BH513513
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T60367
AJ478560
AJ478560
AJ432574
BE730257
BJ219877
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BI562582
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BI510096
BI545634
BG717563
BG717465
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BG843303
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BG84321
CNS05KQ1
BM03553
BM621560
BM621560
BM578416
AQ575468
BH253181
AW501182
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AM561182
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Pseudomonas aeruginosa
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KEYWORDS
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BZ571326/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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BZ211728 Tetracdon
BM037193 fu84c01.y
                                                                                                                                                      August 27, 2003, 18:01:39; Search time 2272.12 Seconds (without alignments) 363.693 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           45562784
                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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CNS02SD3
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AA739600
                                                                                                                   using sw model
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em_gss_inv:*
em_gss_pln:*
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gb_gssl:*
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Maximum DB seq length: 2000000000
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em_gss_phg:*
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gb_est5:*
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em_gss_mam:*
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Match Length DB
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B1562582 603256515 BG911254 603807519 B1910096 603067939 B1546534 603187842 BG717956 602698932 BF984839 602308094

BI866970 ft67a07.x BG424809 602453459 BG335538 602403831

BG717465 602689226 BU594473 AGENCOURT BU500183 AGENCOURT CD58712 AGENCOURT AL296288 TETRAGON BU193557 AGENCOURT

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Gaps

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Length 910; Indels

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/dev_stage="4-5 month"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="condition of the condition of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (Dases I to 438).
Clark, M. Johnson, S. L., Lehrach, H., Lee, R., Lit, F., Marra, M., Eddy Clark, M. Johnson, S. L., Lehrach, H., Beck, C., Wylle, T., Underwood K., Steptoe, M., Thesing, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., Waterston, R., Washu Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                            BM037193 438 bp mRNA linear EST 05-NOV-2001 fu84c01.yl Gong zebrafish ovary Danio rerio cDNA clone IMAGE:5377536 5' similar to SW:PMA2_HUMAN 015305 PHOSPHOMANNOMUTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Actinopterygil; Neopterygil; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://gar.me.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Blological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The library was constructed by Dr. Z. Gong. DNA Sequencing by: Washington Dniversity Genome Sequencing Center St. Louis. Please contact Zhiyuan Gong for further information on this library (National University of Singapore, Department of Biological Sciences, Lower Kent Ridge Road, Singapore 119260). High quality sequence stop: 323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                       Score 23.4; DB 29;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23; DB 12;
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243
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/organism="Danio rerio"
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/db_xref="taxon:7955"
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221
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BM037193
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81.8%;
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BM037193/c
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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AUTHORS
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRX cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis genome survey sequence FUC-Ori end of clone 16,172 of library G from Tetraodon nigroviridis, genomic survey sequence.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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/note="Genoscope sequence ID : COAG161DE11SP1-end :
PUC-Ori"
                                                                                                                                                  /clone="msh2_1835"
/clone_11b="msh"
/note="Environmental isolate. Whole genomic shotgun
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                                                                                                                                                                                                                                                                                                                                                                        Length 802;
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/mol_type="genomic DNA"
/db_xref="taxon:99883"

    802
    /organism="Pseudomonas aeruginosa"

                                                                                                                                                                                                                                                                                                                                                                        71.8%; Score 24.4; DB 29;
82.4%; Pred. No. 1.6e+02;
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                                                          /mol_type="genomic DNA"
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                                                                                       /strain="mSH"
/db_xref="taxon:287"
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Tetraodon nigroviridis
Tetraodon nigroviridis
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EST 23-APR-2001
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases I to 704)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Vlan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota: Metazoa: Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 603)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
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Plate: 107 row: G column: 4
High quality sequence stop: 488.
Location/Qualifiers
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MR07776. Sprime GM Drosophila melanogaster ovary BlueScript
Drosophila melanogaster cDNA clone GM10776 Sprime similar to
X78555: calpA FBGN0012051 PID:9562289 SWISS-PROT:011002, mRNA
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Pred. No. 6.7e+02;
0; Mismatches 4; Indels 0;
                                                                                                                                                        TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Email: whitelaw@tigr.org
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/organism="Drosophila melanogaster"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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/db_xref="taxon:7227"
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                                                                                                                      Unpublished
Contact: Cathy Whitelaw
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86.2%;
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Class: sheared ends
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25; Conservative
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/clone_lib="PtIRG2"
/clone_lib="PtIRG2"
/clone_lib="PetCr: lambda ZAP; Site_l: ECORI; Site_2: XhoI;
/note="VectCr: lambda ZAP; Site_l: ECORI; Site_2: XhoI;
/the tissue was harvested in spring and summer from branches
of seed orchard trees which are clones of the same
genotype. Branches were 4-6 inches in diameter. The cDNAs
were directionally cloned into Lambda Zap and were
rescued as a Bluescript derivative in the EcoRI and XhoI
sites.
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Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
Kinlaw.C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Faat: case27w007.pswfs.gov
The sequence entry for this EST has been reverse complimented and
is being submitted in the sense orientation.
Seq primer: M13_Universal.
Location/Qualifiers
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                              Gaps
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USDA IFG Dendrome Project
Institute of Forest Genetics
Dendrome Project, Institute of Forest Genetics, P.O. Box 245,
Berkely, CA 94701
Tel: 5105596429
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                                                                                                                                                                              AA739600
365 PtIFG2 Pinus taeda cDNA clone 8604M 3', mRNA sequence.
AA739600
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            Pred. No. 4.3e+02;
0; Mismatches 5;
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/mol_type="mRNA"
/db_xref="taxon:3352"
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                                                                                                                                                                                                                                                                                              Pinus taeda (loblolly pine)
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CC011462.1 GI:29392738
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          Best Local Similarity 83.9%;
Matches 26; Conservative
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids
                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 180)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3702"
/clone="shix_034371"
/clone="shix_034371"
/clone="shix_034371"
/clone="shix_034371"
/clone="pdr was performed on Arabidopsis thaliana lines each of which contains one or more TPDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
a 45 c 38 g 55 t
                                                                                                                                                                             GSS 04-JAN-2002
                                                                                                                                                                        BH613513
SALK_034371 Arabidopsis thaliana TDNA linear GSS 04-JAN-200 thaliana genomic clone SALK_034371, genomic survey sequence.
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g20480. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/organism="Arabidopsis thaliana"
/Mol_type="genomic DNA"
/strain="Columbia 0"
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83.3%; Pred. No. /...
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                                                  545 CGATIGCIGGCIACIGGCIGCAGCIGC 571
     1 CGATTCTTTGCTACTGGCTGCAGCTGC 27
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hes 25; Conservative
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/dev_stage="0 to 24 hours mixed stage embryonic"
/dev_stage="10 to 24 hours mixed stage embryon BlueScript"
/clone_lib="Lub Drosophila melanogaster embryo BlueScript"
/clone_lib="Lub Drosophila melanogaster embryo BlueScript"
/site_2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dT-primed and directionally cloned at
Book and Andrea and Andrea and Book and Synthesis Kit. Oligo dT-primed and directionally cloned at
Book and 128 g 122 t
/lab_host="SOLR"
/clone_lib="GM Drosophila melanogaster ovary BlueScript"
/note="Grogan: ovary; Vector: BlueScript SK; Site_1: BcoRI;
Site_2: Xhol; Constructed using Stratagene Zab-cDNA
Synthesis kit. Oligo dT-primed and directionally cloned at
EcoRI and Xhol in BlueScript SK(+/-)"
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1 (bass 1 to 611)

1 (bass 1 to 611)

Rarvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
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hit genomic AE003550: arm:3L [9682134,9979619]
estimated-cyto:6701-6709: 04/10/2001
plate: LD.182 row: F column: 1
High quality sequence stop: 500
POLYA-No.
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                     DB 9; Length 603;
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="BDGP_BST:BDCln017400"
/db_xref="taxon:7227"
/clone="LD18261"
                                                                                                                                                                                                                                ch 65.3%; Score 22.2; DB 9;
1 Similarity 88.9%; Pred. No. 8.9e+02;
24; Conservative 0; Mismatches 3
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Unpublished
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Matches 24; Conserv
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Hordeum vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 480)
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Email: est@watson.wustl.edu
High qality sequence stops: 209
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: MI3Rp1
High quality sequence stop: 209.
Location/Qualifiers
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P.O.Box 56 (Vilkinkaari 6A), University of Helsinki FIN-00014,
Finland.
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Barley EST's
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Pred. No. 1.2e+03;
0; Mismatches 7; Indels (
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/db_xref="taxon:4513"
/clone="50001100114004F1"
/dev_stage="Developing seed"
/clone_lib="800011"
/note="12,15,18 days after pollination"
4 a 171 c 137 g 78 t
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/organism="Hordeum vulgare"
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                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="GDB:498242"
/db_xref="taxon:9606"
/clone="IMAGE:78497"
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Institute of Biotechnology
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AJ478560.1 GI:21194515
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78.88;
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88.5%;
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Best Local 5
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(bases 1 to 320)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Rucha, T., Lacy, M., Le, M., Ce, N., Mardis, E., Moore, S., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underryood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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DDNA clone
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yb90h09.rl Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:78497 5' similar to gb:J04449 CYTOCHROME P450 IIIA4 (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="txxxx:370""
/db_xref="txxxx:370""
/clone="SALK_010491"
/clone="pcR was performed on Arabidopsis thaliana lines
ach of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols ach
be found at http://signal.salk.edu/tdna_protocols.html"
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 196)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,E., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                                                                                              This is single pass sequence recovered from the left border of TDNA. This sequence lies within an intron of At1920480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
Washington University School of Medicine
Washington Eark Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 196;
                                                                                                                                                         Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Fax: 858 453 4100 x1/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
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8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
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Pred. No. 8e+02
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/strain="Columbia 0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 64.7%;
1 Similarity 83.3%;
25; Conservative (
                                                                                                                                                                                                                                                                                             Email: ecker@salk.edu
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/diches ThAGES: 382299*
/tissue_type="melanotic melanoma"
/lab_host="BillOB (phage-resistant)"
/clone_lib="NIH_WGC_200"
/note="Organ: skin; Vector: poTB7; Site_1: XhoI; Site_2: BcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI.AhoI sites using the following 5' adaptor: GGORGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of: California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BJ219877 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum cDNA clone wh17g09 3', mRNA sequence.
BJ219877 GI:19958527
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203 c 147 g 162 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 667;
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National Institute of Genetics
111 Tata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.1%; Score 21.8; DB 10; 78.8%; Pred. No. 1.3e+03;
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/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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Ogihara,Y. and Murai,K.
Stressed genes in Triticum aestivum
Unpublished
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
Plate: LLCM511 row: b column: 08
High quality sequence stop: 667.
Location/Qualifiers.
                                                                1. .667
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum (bread wheat)
                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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BJ219877/c
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta; Liliopsida, Poales; Poaceae, Pooideae, Triticae, Hordeum.

1 (bases 1 to 509)
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                                                                                                                                                                  AJ432574 500011 Hordeum vulgare CDNA clone S0001100156511F1, mRNA
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MIH MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute of Biotechnology
University of Helsinki
P.O.Box 56 (Vilkinkaari 6A), University of Helsinki FIN-00014,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Hordeum vulgare"
/mol_type="mkNn"
/db_xref="taxon:4513"
/clone="80001100156B1F1"
/dev_stage="Developing seed"
/clone=11b="800011"
/clone=12,15,18 days after pollination"
i a 176 c 142 g 87 t
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Pred. No. 1.2e+03;
0; Mismatches 7;
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                                            2 GATTCTTTGCTACTGGCTGCAGCTGCAGCCCCG 34
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Tissue Procurement: ATCC/DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                              AJ432574
AJ432574.1 GI:19521026
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78.8%;
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Homo sapiens
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                                CNSO4FD7 904 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 106E22 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                              Al288196.1 GI:8026722
AL288196.1 GI:8026722
AL288196.1 GI:8026722
GS: genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygli; Neopterygli; Teleostei; Suteleostei; Neoteleostei;
Acathomorpha; Acathopterygli; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                     Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviidis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
10835645
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/rione="Genoscope sequence ID : COBG106BC11LP1-end : T7"
/note="Genoscope sequence ID : COBG106BC11LP1-end : T7"
210 c 236 g 217 t 4 others
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Direct Submission
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 27, 2003, 18:00:44; Search time 536.538 Seconds (without alignments) 1372.452 Million cell updates/sec Run on:

US-10-085-612-1 18 Title: Perfect score:

1 gacaagggcaggacagag 18 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

5777422 Total number of hits satisfying chosen parameters:

2888711 seqs, 20454813386 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database

gb_ro:* gb_sts:*

em_fun:* em_hum: em ba:q1 em_mu:

em_om: em_or: em_pat

em_sts: em_un:* em_vi:* em_ph:; em_ro:

em_htg_hum:*
em_htg_inv:*
em_htg_other:* em_htg_mus:

em_htg_pln: *
em_htg_rod: *
em_htg_mam: * em_htg_vrt:*

em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

the number of results predicted by chance to have a Pred. No. is

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AC114884 Rattus no	3733 Mus mus	37 Ratt	052	Mus mus	Mus	Mus	Bos t	ACUZO/OL MUS MUSCU	Mus	2 Mus	Ratt	Mus mus	Rattus n	B Mus mu	Rattus n	Rattus	Mus mus		Capra h		S209P628	birone d	HOMO	3 Homo sap	9 Homo sap	mo sap	n (17	mo sa	AXBUUS8b Sequence		200	30 S	74359 Mus m	Γ	531 Rattus n	inuation (13	912 Homo s 294 Homo s	1
ID	AC11488	AC11873	AC129737	AC10305	AC11988	AC12405	AC12135	AC14488	AC14518	AC13840	AC0790	AC13203	AC13567	AC098104	AC0798	AC12320	ACTO024	AC131229	AR22290	CHI2920	HSA29598	G95069	AKI4 ZI4	AC00612	AC13843		AC110286	AL92909	AC13635	AABOUDS	AT.7306	AT.354891	AC00458	AC0743	AC07412	AC108631_0		AC015912 AC069294	
% Query Match Length DB	00.0 144869	00.0 188490	00.0 196662	00.0 203/08	00.0 244620	4.4 47589	4.4 116608	4.4 151613	4.4 1034/3	4.4 196351	4.4 205621	4.4 217181	4.4 219937	4.4 237330	4.4 238658	4.4 239553	4.4 287536	4.4 347924	1.1 29	1.1 532	1.1 573	1.1 590	1 1 0000	32735	1.1 38016	1.1 38235	1.1 60271	1.1 62915	1.1 64706	1.1 /5250	1 1 88592	1.1 103706	1.1 104871	1.1 106041	1.1 108195	1.1 110000	1.1 110000	91.1 118172 9 91.1 123778 9	
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ALIGNMENTS

RESULT 1 AC114884 LOCUS DEFINITION

AC114884 110ear HTG 25-SEP-2002 Rattus norvegicus clone RP31-557J15 strain Brown Norway, WORKING DRAFT SEQUENCE, 8 ordered pieces. AC114884.2 GI:23308021 HFG; HFGS_PHASE2; HFGS_DRAFT. Rattus norvegicus (Norway rat) Rattus norvegicus ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE AUTHORS

Rattus. 1 (bases 1 to 144869) Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,

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BASE COUNT
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Denjamin, B., Blakesley, R. W., Bouffard, G.G., Brinkley, C., Brooks, S., Caridga, K., Coleman, B., Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Han, J., Han, J., Hansen, N., Ho, S., L., Idol, J. R., Karlins, B., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q. L., Maduro, V. B., Margulies, E. H., Masiello, C., Maskeri, B., McCloskey, V. C., McDowell, J., Paquirigan, C., Schueler, M. G., Sison, C., Stantripop, S., Thomas, J. W., Thomas, P. J., Fouchman, W. W., Todron, W. Walker, M., Wetherby, K. D., Wiggins, L., Yough, J., L. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 8 configs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 4966: config of 4966 bp in length 4907 74022: contig of 4956 bp in length 74023 74122; gap of unknown length 74023 7637: contig of 24956 bp in length 7637: contig of 2515 bp in length 7638 76737: gap of unknown length 76738 8254: contig of 5787 bp in length 76738 8254: contig of 5787 bp in length 82555 82524: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                  Green.E.D.
Direct Submission
Direct Submission
Submitted (25-SEP-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Sep 25, 2002 this sequence version replaced gi:19387611.
                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (13-MAR-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 144869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: NIH Intramural Sequencing Center
Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@hdgri.nih.gov
------- Project Information
Center project name: cxn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: 557J15
                                                                                                                                                                                                                                                           (bases 1 to 144869)
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COMMENT

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Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S. M.,
Akhter, N., Antonellis, A., Ayele, K., Bockstrom-Sternberg, S. M.,
Benjamin, B., Blakesley, R., Bouffard, G.G., Breen, K., Brinkley, C.,
Brooks, S., Dietrich, W.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J. R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, Q. L., Maduro, V. B.,
Margulies, E. H., Masiello, C., Maskeri, B., Mastrian, S. D.,
McCloskey, J. C., McDowell, J., Pagnirigan, C., Pearson, R.,
Portnoy, M. E., Prasad, A., Schueler, M. G., Stantripop, S., Thomas, J. W.,
Thomas, P. J., Touchman, J. W., Tsurgeon, C., Vogt, J. L., Walker, M. A.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus clone RP31-385022 strain Brown Norway, WORKING
PRAFT SEQUENCE, 4 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RF31"
1. .59406
/note="clone overlaps with GenBank Accession Number
AC114881 clone RP31-385022 (center project name cxo)"
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99342: coutig of 16718 bp in length
943: 99442: gap of unknown length
110906: contig of 11464 bp in length
1007 121200: contig of 10194 bp in length
121300: gap of unknown length
121300: gap of unknown length
131300: gap of unknown length
144869: contig of 23569 bp in length
10cation/Qualifiers
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/strain="Brown Norway"
/db_xref="taxon:10116"
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HTG; HTGS_PHASE2; HTGS_DRAFT.
RATLUS NOTVEGICUS (NOTWAY rat)
RATLUS NOTVEGICUS
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98009. .141249
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Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consists of 4 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 197908: contig of 97908 bp in length

* 97909 98009 141249: contig of 43241 bp in length

* 141250 141349: gap of unknown length

* 141350 168491: contig of 27142 bp in length

* 168492 168591: gap of unknown length

* 168492 168591: gap of unknown length

* 168592 178877: contig of 10266 bp in length.
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. NISC Comparative Sequencing Initiative
                                                                                                                               Direct Submission
Submitted (13-MAR-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 178857)
                                                                                                                                                                                                                                                                 Direct Submission
Submitted (29-JUN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jun 29, 2002 this sequence version replaced gi:19387608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 166000; agarose-fp
Insert size: 178557; sum-of-contigs
Quality coverage: 11.42x in Q20 bases; agarose-fp
Quality coverage: 10.61x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Summary Statistics
Sequencing vector: plasmaid; n/a; 100% of reads
Sequencing vector: plasmaid; n/a; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178011 bases at least Q40
Consensus quality: 178364 bases at least Q30
Consensus quality: 178364 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                       Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP31-385022"
/clone_lib="RP31"
1. .97908
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: cxo
Center clone name: 385022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                            (bases 1 to 178857)
                                                     Unpublished
                                                                                                           Green, E.D
                                                                                                                                                                                                                                             Green, E.D
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                                                                                                                                  TITLE
JOURNAL
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AUTHORS
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JOURNAL
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AL Unpublished

2 (bases 1 to 188490)

8 birtan, L. Linton, L. Nusbaum, C., Lander, E., Ali, A., Allen, N.,

8 birtan, S., Linton, L., Nusbaum, C., Bloom, T., Boyslavkiy, L.,

8 boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,

8 cook, A., Cooke, P., DeArtlano, K., Dewar, K., Diaz, J. S., Dodge, S.,

8 cook, A., Cooke, P., DeArtlano, K., Dewar, K., Diaz, J. S., Dodge, S.,

8 cook, A., Cooke, P., FitzHugh, W., Gape, D., Galagan, J., Gardyna, S.,

8 cook, A., Cooke, P., FitzHugh, W., Gape, D., Galagan, J., Gardyna, S.,

8 cook, A., Karatas, P., FitzHugh, W., Gage, D., Calagan, J., Gardyna, S.,

8 cands, S., Rerreira, P., FitzHugh, W., Lawar, K., Diaz, J. S.,

8 candas, R., Maratas, A., Kells, C., LaRocque, K., Lamazares, R.,

8 candars, T., Lehoczky, J., Levine, R., Lindblad, T.Ohnson, R., MacGarthy, M., McEnan, P., Marquis, N., Matthews, C.,

McCarthy, M., McEnan, P., Mayor, J., Marquis, N., Matthews, L.,

8 McCarthy, M., McEnan, P., McKernan, K., Meldrim, J., Meneus, L.,

8 McCarthy, M., McEnan, P., Murphy, T., Naylor, J., Nigoyen, C., Nicol, R.,

8 Nord, C., Norman, C.H., O'Comnor, T., O'Donnell, P., O'Neil, D.,

9 cliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,

8 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuper, S., Schuper, S., Schuper, S., Schuper, S., Schuper, S., Schuper, S., Norman, M., Travis, N., Waynan, J., Ye, Yo, A., Wilson, B., Wu, X., Waynan, J., Ye, Yo, A., Wilson, B., Wu, X., Waynan, J., Ye, W.J., Young, G.,

8 Zainoun, J., Yoo, A., Wilson, B., Wu, X., Waynan, S., Theodore, J.,

8 John, J., Yoo, A., Wilson, B., Wu, X., Waynan, S., Waynan, S., Seve, J., Waynan, S., Raynan, S., Seve, W., Waynan, S., Raynan, Wayn, S., Waynan, S., Waynan, S., Waynan, S., Waynan, A., Waynan,
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Mus musculus clone RP24-170A20, WORKING DRAFT SEQUENCE, 3 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boustlavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
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Mammalla; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 188490)
Bairren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-170A20
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                                                                                                                                                                                                   (center project name cxn)"
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98009. .141249
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//note="assembly_fragment"
//note="clone overlaps with GenBank Accession Number
AC114884 clone RP31-557J15 (center project name cxn)
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//note="assembly_fragment"
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65;
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42335 c 42524 g 45938 t
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Pred. No. 6
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Mus musculus
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AC118733.3 GI:28467248
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Rattus.
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                         RESULT 4
      DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
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Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad-Tob, K., Liu, G., Lui, A., Mabbitt, R., MacLen, C., Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., Maddrim, J., Menels, L., Mihova, T., Mathews, C., McCarthy, M., Muyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, R., Phunkhang, P., Pierre, N., Rachupka, A., Ramasany, D., Raymond, C., Retta, R., Sever, P., Sohuere, S., Schuere, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-FBB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Feb 22, 2003 this sequence version replaced gi:28209706. Anl repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: 125111
Center clone name: 170.8_20
Center clone name: 170.8_20
Center clone name: 170.8_20
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Nye-terminator BMS Dys; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 187861 bases at least Q40
Consensus quality: 188043 bases at least Q30
Consensus quality: 188126 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 18300; squrose-fp
Conting coverage: 11.4 in Q20 bases; squrose-fp
Quality coverage: 11.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of M. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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9910: gap of 100 bp
113719: contig of 103809 bp in length
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188490: contig of 74671 bp in length.
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1. .9810
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57443 a 38263 c 37627 g 54957 t
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/note="assembly_fragment"
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/note="assembly_fragment
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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vector_side:left"
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12. 1 (Lases 1 to 196662)
12. Allen, H., Alsbrooks S., Amin, A., Angulano, D., Angulano, D., Angulano, D., Angulano, D., Barder, M., Banastead, M., Benbmed, P., Barder, M., Estaro, M., Ballar, J., Blaireburg, R., Blyth, P., Brown, M., Blando, M., Blair, J., Blaireburg, R., Blyth, P., Brown, M., Bryant, M., Bulhay, C., Carter, R., Caraco, I., Ceasar, H., Center, A., Cherer, A., Cherer, M., Chereland, C., Cockell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Lay, B., Davila, M., Divya, K., Detagor, D., Chenson, S., Denamo, C., Ding, Y., Dinh, H., Divya, K., Davila, M., Escotto, M., Eugene, C., Byans, C.A., Falls, T., Ran, G., Franandez, S., Planda, A., Durbin, K., Duva, B., Baves, K., Egan, A., Escotto, M., Eugene, C., Byans, C.A., Carter, M., Gabla, A., Canter, M., Garter, M., Gabla, A., Canter, M., Garter, M., Garter, M., Gabla, A., Canter, M., Garter, M., Mander, M., Marter, G., Mall, M., Carter, M., Marter, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, 
                                                                                                                                                                                                                                                                                                                                                                                                                                          AC129737 196662 bp DNA linear HTG 08-OCT-2002
Rattus norvegicus clone CH230-506G1, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                Gaps
                                                                                            .;
0
DB 2; Length 188490;
65;
                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                0; Mismatches
                100.0%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                      28760 GACAAGGCCAGGACAGAG 28743
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                Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

AUTHORS TITLE REFERENCE

JOURNAL

COMMENT

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Research, 20 Cincles, Cambridge, Mr. Villi, USA, Ribarson, S. Birren, B., Musbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barná, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barná, N., Bastien, V., Bloom, T., Boukhqalter, B., Camarata, J., Chaepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Doleg, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerad, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Macdonald, P., Major, J., Manbitt, R., Maclean, C., Macdonald, P., Major, J., Manbing, J., Matthews, C., McCarthy, M., Mullow, J., Meneus, L., Mihova, T., Matthews, C., McCarthy, M., Nayyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, Y., Peterson, R., Phunkhang, P., Pierre, N., Ramond, C., Rayon, P., Santh, C., Schupback, R., Seaman, S., Schupback, R., Seaman, S., Schupback, R., Stanger-Thoman, N., Stojam, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Vash, R., Wilson, B., Wu, X., Vassiliev, H., Venkataraman, V. S., Vash, R., Wilson, B., Wu, X., Vassiliev, H., Venkataraman, V. S., Vash, R., Wilson, B., Wu, X., Vassiliev, H., Venkataraman, V. S., Vash, R., Wilson, B., Wu, X., Vassiliev, H., Venkataraman, V. S., Vash, R., Wilson, B., Wu, X., Vassiliev, H., Wenkataraman, V. S., Vash, R., Wilson, B., Wu, X., Vassiliev, H., Wenkataraman, V. S., Vash, R., Wilson, B., Wu, X., Vassiliev, H., Wenkataraman, V. S., Vash, R., Wilson, B., Wu, X., Vash, R., Wallon, M., Wash,                                                                                                                                   AC101931 209706 bp DNA linear HTG 04-JUN-2003
Mus musculus clone RP24-63023, *** SEQUENCING IN PROGRESS ***.
AC101931
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Submitted (04-JUN-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tophama, K., Travers, M., Travis, N., Triavis, Y., Taravers, M., V., Valla, V., Vassiliev, H., Valla, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-Nov-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.gene.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 209706)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP24-63023
114096 GACAAGGCCAGGACAGAG 114079
                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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ORGANISM
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Submission

Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA

On Sep 14, 2002 this sequence version replaced gi:22538766.

The sequence in this assembly is a combination of BAC based reads and whole genome shortgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence ends will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bom.tmc.edu/docs/denbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is balleved to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* The accession number will be preserved.

* The accession number will be preserved.
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                                                                                                                                                                                      Submitted (02-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
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51858 a 40862 c 42866 g 54119 t
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                                                                                                                                                                                                                                                                                                                                Rat Genome Sequencing Consortium.
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Weinstock, G. and Gibbs, R.A.
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                                                                                               (bases 1 to 196662)
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Best Local Similarity 100.0
Matches 18; Conservative
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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64;
                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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AC103052.5 GI:30580047
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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                                                                                                                                  Center project Information
Center project name: L17758
Center clone name: 63_0_23
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of Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced g1:23614691.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the Feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma.J.,
Mansheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,B., Mapudartne,M., Mahmoud,M., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Midosayljeric,A., Miner,G., Midja,B., Montemayor,J., Moore,S.,
Moorgan,M., Morris,R., Mineris,S., Munidasa,M., Murphy,M., Nair,L.,
Nanokelmen,D., Okwonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Rajer,R.,
Reilly,B., Reilly,M., Rechlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Rose,M., Rose,R., Ruiz,S.J.,
Shatty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Steimle,M., Strong,R., Sutten,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,M., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldcon,L., Walker,B., Wang,J.,
Walght,D., Wright,R., Warren,J., Warren,R., Woll,C., Walliams,G., Willson,R., Welsey,R., Wooden,H., Wooley,R.,
Walst,C., Welsey,R., Sutton,X., Zhao,S., Dunn,D., Yoon, N.,
Welnstock,G. and Globs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length

* (See http://www.higsc.bom.tmc.edul/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 212164 bases at least 040
Consensus quality: 213776 bases at least 030
Consensus quality: 213703 bases at least 020
Estimated insert size: 223883; sum-of-contigs estimation
Quality coverage: 7x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: GJCH
Center clone name: CH230-147P15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Atlas 3.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 217691)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1 to 217691)
Worley, K.C.
Direct Submission
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Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., DeArallano, K., Diaz, J.S., Doode, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, M., Tilev, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Marbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Minou, T., Mandya, V., Murphy, T., Naylor, J. Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Najor, J., Peterson, K., Phunkhang, P., Pierre, N., Ramchupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, R., Schauer, S., Schupeac, K., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainou, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON APR 17, 2003 this sequence varsion replaced gi:28629983. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L25016
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contigo of 40455 ~r
gap of 100 bp
-in of 77522 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 8876 bp in length gap of 100 bp contig of 22568 bp in length gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29471 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2154: contig of 2154 bp in length 2254: gap of 100 bp 2921: contig of 667 bp in length 3021: gap of 100 bp 3879: contig of 858 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8876 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of 100 bp
contig of 675 bp in length
gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 2947
gap of 100 bp
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/note="assembly_fragment
clone_end:8P6
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA'/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: 93_G_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06502:
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184125
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Surren, B., Linton, L.,

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,

Anderson, S., Barna, N., Campoplano, A., Chang, J.,

Boukhgaiter, B., Eroun, A., Camarata, J., Campoplano, A.,

Chazaro, B., Choepel, Y., Clangelo, M., Collins, S., Collymore, A.,

Cook, A., Cooke, P., FitzHudh, W., Gage, D., Galagan, J.,

Raro, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R.,

Landers, T., Lehoczky, J., Levine, R., Lindblad, Toh, K., Liu, G.,

MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

MacLariny, M., McEwan, P., McKernan, K., Meldrim, J., Menens, L.,

Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,

Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,

Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pierre, N., Stander, S., Schuuer, S., Volan, Milson, B., Wu, X., Wyman, D., Ye, W., Young, G.,

Viel, R., Volan, Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Viell, R., Volan, Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC119882 244620 bp DNA linear HTG 23-APR-2003
Mus musculus clone RP24-93G1, WORKING DRAFT SEQUENCE, 10 unordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
   are represented as runs of N. The order of the pieces is balieved to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="wgs_contig"
50714 c 51140 q 59960 t
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP24-93G1
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Murphy, T., Naylor, J., Nguyen, C., Nicoll, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phukkhang, P., Pierre, M., Raymond, C., Retta, R., Rise, C., Sogov, P., Soman, J., Schauer, S., Schupback, R., Saman, J., Semen, G., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 28, 2002 this sequence version replaced gi:21360073. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferrelra, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Plerre, N., Hagos, B., Horton, L., Hulme, W., Illev, L., Johnson, R., Jones, C., Kamat, A., Karlasa, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Machen, C., Maddonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This record contains 59 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful
* arbitrary clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* thil be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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Web site: http://www-seq.wi.mit.edu
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhqalter,B.,
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40278
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AC121356 116608 bp DNA linear HTG 16-WAR-2003 Mus musculus clone RP23-52D17, WORKING DRAFT SEQUENCE, 5 unordered pieces.
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, Y., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Diaz, J.S., Dodge, S., Dooley, R., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus mouse)
Mus musculus
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 116608)
Birren, B., Nusbaun, C. and Lander, E.
Mus musculus, clone RP23-52D17
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                         Score 17; DB 2; Length 47589;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                      0; Indels
                           gap of 100 bp contig of 667 bp in length gap of 100 bp contig of 661 bp in length contig of 661 bp in length contig of 661 bp in length gap of 100 bp
                                                                                                                  100 bp
of 777 bp in length
                                                                                                                                             gap of 100 bp
contig of 770 bp in length
                bp in length
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AC121356.3 GI:28975044
HTG; HTGS_PHASE1; HTGS_DRAFT.
   gap of
contig
gap of
                                                                                                                                  contig
gap of
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                                                                                                                                                                                         94.4%; Scc
milarity 100.0%; Pr
Conservative 0;
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43563:
44224:
44324:
44985:
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46732:
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                               12796:
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Best Local Similarity
'...s 17; Conserve
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Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Liddblad, Tob, K., Liu, G., Luid, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nuyuen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Nei, D. D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Kise, C., Rogov, P.,
Rachupka, B., Stange-Thomann, N., Stojanovic, N., Seman, S., Sevary, P., Seman, T., Schauer, S., Schauer, S., Theodore, J., Tophan, K., Travers, M.,
Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M.,
Wans, I., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Whan, D., Youn, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct, Submission
                                                                                                                                                                                                                                                                                                                                 Center Clone name: 52_D_17

Center Clone name: 52_D_17

Sequencing vector: Plasmid; v.; 100% of reads
Sequencing vector: Plasmid; v.; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 115769 bases at least Q40

Consensus quality: 115799 bases at least Q30

Consensus quality: 115995 bases at least Q30

Consensus quality: 116130 bases at least Q20

Insert size: 150000; agarose-fp

Insert size: 15000; sum-of-contigs

Quality coverage: 10.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23731: contig of 23731 bp in length 23811: gap of 100 bp 41019: contig of 17188 bp in length 41119: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60788: contig of 19669 bp in length 60888: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97152: contig of 36264 bp in length 97252: gap of 100 bp 116608: contig of 19356 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seg.wi.mit.edu
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1. 116608
Acranism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/note="assembly_fragment
clone_end:SP6
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/note="assembly_fragment"
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J. (Dases I to 151613)
Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, G., Carlaga, K.,
Chu, G., Coleman, B., Coleman, H., Bngle, J., Granite, S., Guan, X.,
Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P.,
Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q.,
Legaspi, R., Maduro, O.L., Maduro, V.B., Margulies, E.H., Masiello, C.,
Maskeri, B., McDoweal, J., Pagulrigan, C., Pearson, R., Portnoy, M.E.,
Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K.,
Sison, C., Stanttipop, S., Thomas, J. M., Thomas, P. J., Islpourl, V.,
Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
NISC Comparative Sequencing Initiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC144886 151613 bp DNA linear HTG 23-MAY-2003
Bos taurus clone RP42-363322, WORKING DRAFT SEQUENCE, 15 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                      Gaps
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Contact: nisc_zoo@nhgri.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
Center project Information
Center clone name: 363722
Center clone name: 363722
Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Consensus quality: 14755 bases at least 030
Consensus quality: 147591 bases at least 030
Consensus quality: 147291 bases at least 020
Insert size: 120000; agarose-fp
Insert size: 120213; sum-of-contigs
Quality coverage: 11.18x in 020 bases; agarose-fp
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34865 a 23112 c 22833 g 35397 t
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97253. .116608
/note="assembly_fragment
                                                                                                                                                                                                                                          ch 94.4%; Score 17;
1 Similarity 100.0%; Pred. No.
17; Conservative 0; Mismatch
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Bos taurus (cow)
Bos taurus
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AC144886.1 GI:31044305
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Green, E.D.
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Best Local Similarity
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                                                                                                                                     RESULT 11
AC026761
                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
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ORIGIN
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it is available and the accession number will
                                                                                                                                                                                                                                                                    contig of 6224 bp in length
gap of unknown length
contig of 6313 bp in length
gap of unknown length
contig of 11438 bp in length
gap of unknown length
contig of 9408 bp in length
gap of unknown length
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31102 a 44763 c 42876 g 31470 t
                      contig of 2844 by gap of unknown locating of 2180 by gap of unknown locating of 4536 by gap of unknown locating of 4621 by gap of unknown locating of 4621 by gap of unknown locating of 6224 by gap of unknown locating of 6214 by gap of unknown locating of 6214 by gap of unknown locating of 6313 by conting of 6313 by
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70016="assembly_fragment"
30630 . 42067
70016="assembly_fragment"
42168 . 51575
70016="assembly_fragment"
51676 . 62329
70016="assembly_fragment"
52430 . 72849
72950 . 86363
72950 . 86363
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9861. 13071
/note="assembly_fragment"
13172. 17792
/note="assembly_fragment"
17893. 24116
/note="assembly_fragment"
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122806. 151613
/note="assembly_fragment
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/note="assembly_fragment"
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5225. .9760
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/note="assembly_fragment
clone_end:8P6
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/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="RP42-363372"
/clone_lib="RP42"
                                                                                                                                                                                                                                                contig
gap of c
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100096. .122705
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Grills, G., Han, J., Montgomery, K.T., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R. Gordon, M., Goltz, J.S. and Kucherlapati, R. Direct Submission Bear State of Medicine Genome Center, 1300 Morris Park Ave., Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Enstein College of Medicine Genome Center, 1300 Morris Park Ave., Enstein College of Medicine Genome Center, 1300 Morris Park Ave., Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Enstein College of Medicine Genome Center, 1300 Morris Park Ave., Grills, G., Han, J., Montgomery, K.T., Lee, E., Long, J., Pomerantz, R., Gordon, M., Goltz, J.S. and Kucherlapati, R., Direct Submission Submission Submission Submission Submission Submission Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC026761 163475 bp DNA linear ROD 21-SEP-2002 Mus musculus Strain 12956/SvEvTac chromosome 19 BAC, RP22-325422,
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Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,
Ioshikhes,I.P., Shin,C., Decker,J., Thomas,E., Perera,A.,
Gordon,M., Goltz,J.S. and Kucherlapati,R.
Direct Submitseion
Submitted (21-SEP-2002) Harvard Partners Center for Genetics and
Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
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Grills, Han, J., Montgomery, K.T., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R.
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                                                                                                                           Gaps
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                                                                                                                           0;
Length 151613;
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Contact: hpgc@mendel.mgh.harvard.edu
                                                                                                                           Indels
Query Match
94.4%; Score 17; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0;
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Mus musculus
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join(15583. 17616,17873. 17998,18090. 18181,18407. 18494,
18682. 18787,19500. 19578,20990. 21049,25606. 22738,
56014. .26114,26510. .26802,27450. .27561,2924. .29514)
fproduct="AB072976 Mus musculus D5D mRNA for delta-5
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                                                                                                                    /rpt_family="L2"

join(88564. 8683,11390. .13371)

join(88564. 8620325 Mus musculus, clone MGC:28169

IMAGE:3985840, mRNA, complete cds"

complement(9830. .9582)

join(9830. .9582, 39927,154245. .154609,
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rpt_famly="MT2A"
complement(1471. .14534)
/rpt_famly="BlF" .1554)
/rpt_famly="BlF" .15541)
/rpt_famly="BlA"
join(15883 .17616,17873 ...
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complement(20118. .20270)

/rpt_family="RSINE1"

/rpt_family="845" .20415)

/rpt_family="846" .20529 .20612
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10990. 111730
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/rpt_family="B4"
24229. .24294
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20080. .20108
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/rpt_family="PB1D10"
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/rpt_family="ID4"
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complement(21436. .21636)
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2753. .12867
/rpt_family="ID_B1"
6934. .6952
/rpt_family="ID4"
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1770. 21700
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2631. .23002
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                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                           mRNA
                    STSS are identified using ePCR (Genome Res. 7:541-550).
Repeats are identified using RepeatWasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Regions of sequence similarity are identified by BLAST and CDNA sequences in Unique. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                               SEQUENCING READ COVERAGE: Attempts are made to complete double strandedsequence for all regions. All sequence is completed to a standard of coverage with a minimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the amnotation aslow Coverage. Low coverage linkages are verified by PCR product size verification or verification of forward and reverse reads from chones which span
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standars - estimated average error rate is less than 1 per 10,000 bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: ACD Sequencing vector: pUC18, L08752, 36%; pSMART, AF399742, 64% Sequencing vector: pUC18, L08752, 36%; pSMART, AF399742, 64% Assembly program: phrap version 0.990319
Contig length: 163475
Fraction of Phrap value < 40: 0
Error Rate in Consed: 0.01 per 10,000 bases
Number of N's in consensus: 0
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Phrap Value Range
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/rpt_family="RSINE1"
complement(6398. .6582)
/rpt_family="B4"
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/rpt_family="B4"
6849. .6868
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/rpt_family="B1_MM"
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/chromosome="19"
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5605. .5715
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6869. .6933
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f unknown length
g of 12067 bp in length
unknown length
g of 11022 bp in length
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a 52193 c 51596 g 34827 t
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/note="assembly_fragment"
14981. .18347
/note="assembly_fragment"
18448. .26843
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43292. .55753

/note="assembly_fragment"

55854. .67920

/note="assembly_fragment"

68021. .79042
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/note="assembly_fragment"
26944. .33499
/note="assembly_fragment"
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/note="assembly_fragment"
9412. .11916
/note="assembly_fragment"
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/note="assembly_fragment"
1913. .9311
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108039. .125825
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2588. .4812
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/mol_type="genomic DNA"
/db_xref="taxon:9913"
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/clone_lib="RP42"
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125926. .173362
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Matches 17; Conservative
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33233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. (Dases 1 or 17352)
Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Chu, G., Chu, C., Brooks, S., Cariaga, K., Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J. R., Karlins, E., Kwong, P., Laric, P., Lee-Lins, S.-Q., Hurle, B., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Mastello, C., Maskeri, B., McDowell, J., Paquirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J., W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K. D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                 HTG 12-JUN-2003
                                                                                                                                                                 AC145188 173362 bp DNA linear HTG 12-JUN-200
Bos taurus clone RP42-483023, WORKING DRAFT SEQUENCE, 16 unordered
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center Close name: 483023
Center Close name: 483023
Sequencing vector: plasmid; n/a: 100% of reads
Sequencing vector: plasmid; n/a: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 168014 bases at least Q30
Consensus quality: 169811 bases at least Q30
Consensus quality: 169811 bases at least Q30
Insert size: 158000; agarose-fp
Insert size: 171862; sum-of-contigs
Quality coverage: 10.07x in Q20 bases; sum-of-contigs
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: gap of unknown length
: contig of 2225 bp in length
: gap of unknown length
: contig of 4399 bp in length
: gap of unknown length
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Bos taurus (cow)
Bos taurus
        125435 ACAAGGCCAGGACAGAG 125451
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                                                                                                                RESULT 12
AC145188/c
                                                                                                                                                                                           DEFINITION
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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RESULT 13 AC138402/c

DEFINITION

ACCESSION KEYWORDS

VERSION

ORGANISM

TITLE JOURNAL REFERENCE AUTHORS

REFERENCE

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AC079082 205621 bp DNA linear ROD 15-NOV-2002 Mus musculus chromosome 10 clone rp23-161b11 strain C57BL/61,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
musculus
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 205621)
2 King.F. and Roe, B.A.
Mus musculus BAC Clone rp23-161b11
                     Center Clone name: 263_0_11

Center Clone name: 263_0_11

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 19546 bases at least Q40
Consensus quality: 196011 bases at least Q30
Consensus quality: 196126 bases at least Q30
Consensus quality: 196126 bases at least Q30
Insert size: 192000; agarose-fp
Insert size: 196151; sum-of-contigs
Quality coverage: 12.1 in Q20 bases; agarose-fp
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 11993: contig of 11993 bp in length
12093: gap of 100 bp
4 76435: contig of 64342 bp in length
75535: gap of 100 bp
196535: contig of 119816 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RPCI-24 Male Mouse BAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector_side:right"
56384 a 40543 c 40822 g 58402 t
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/note="assembly_fragment"
76536. .196351
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/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .196351
/organism="Mus musculus'
/mol_type="genomic DNA"
/db_xref="taxon:10090"
Center project name: L28846
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Best Local Similarity 100.(
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete sequence
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Submitted (29-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (Dases 1 to 196351)

Birran,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,

Butten,B., Acachchi,B.M., Barna,N., Bastian,V., Bloom,T.,

Boguslavkiy,L., Boukhgalter,B., Canam,B., Chang,J., Choepel,Y.,

Collymore,A., Cook,P., Cooke,P., Corum,B., DeArellano,K.,

Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Brickson,J., Faro,S.,

Ferreira,P., FitcGerald,M., Gage,D., Galagan,J., Gardyna,S.,

Graham,L., Grand-Pierre,N., Hafez,N., Hagoplan,D., Hagos,B.,

Hall,J., Horton,L., Hulm,W., Illev,I., Johnson,R., Jones,C.,

Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,K., Jones,C.,

Macdonald,P., Major,J., Manning,J., Mathews,C., McCarthy,M.,

Meldrim,J., Meneus,L., Mihova,T., Matheys,C., McCarthy,M.,

Meldrim,J., Manous,L., Manning,J., Matheys,C., McCarthy,N.,

Neldrim,J., Manous,L., Phukkang,P., Plerre,N.,

Rachupka,A., Ramasamy,U., Raymond,C., Phukkang,P., Plerre,N.,

Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,

Roman,J., Schauer,S., Schupback,R., Severy,P., Smith,C.,

Spencer,B., Schauge-Thomn,N., Stubbs,M.,

Talamas,J., Teosfaye,S., Thecdore,J., Topham,K., Travers,M.,

Nyman,D., Young,G., Zahnon,N., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dipublished

2 (bases 1 to 196351)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barra,N., Bastien,V., Balom,T., Boguslavkiyi... Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,X., Collymore,A., Cook,A., Cook,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzderald,M., Gage,D., Galagan,J., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jafez,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Inidblad-Tob,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Seaman,S., Severy,P., Samith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Tavers,M., Vasland, A., and Sody,M. Direct Submission, D., Young,G., Zainoun,J., Zolmek,L., Zimmer,A. and Sody,M. Direct Submission
                                                                                            AC138402 196351 bp DNA linear HTG 07-MAR-2003
Mus musculus chromosome 14 clone RP24-263011 map 14, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bassa, 1 to.196351)
Birren, B., Nusbaun, C. and Lander, E. Mus musculus chromosome 14, clone RP24-263011
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On Mar 7, 2003 this sequence version replaced gi:28461005.
All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---- Project Information
                                                                                                                                                               SEQUENCE, 3 unordered pieces.
                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
                                                                                                                                                                                                                                   AC138402.3 GI:28876093
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TITLE JOURNAL REFERENCE

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Gaps

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TITLE JOURNAL

COMMENT

Length 196351;

200 others

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Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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/clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"
52129 a 53223 c 50420 g 49849 t
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                                                                                                                                                                                                                                                                                                                                                                            S. (bases 1 to 205621)
Ying,F. and Roe,B.A.
Direct Submission
Submitted (15-NOV-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                      Direct Submission Submitted (04-MAY-2002) Department Of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                         Direct Submission Submission Submitted (07-MAX-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                             Submitted (18-AUG-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACL32033 217181 bp DNA linear HTG 19-NOV-2 WACTUS NOTVEGICUS CLONE CH230-127G19, WORKING DRAFT SEQUENCE, 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
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/chromosome="10"
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AC132033.4 GI:25091414
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Unpublished
2 (bases 1 to 205621)
Ying, F. and Roe, B.A.
Direct Submission
                                                                                                                                                                                                                                                    OK 73019, USA 4 (bases 1 to 205621)
Ying, F. and Roe, B.A.
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                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
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AL Submitted (29-AUG-2002) Human Genemic Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(Dases 1 to 217181)

Rat Genome Sequencing Consortium.

Direct Submission

AL Submitted (19-NOV-2002) Human Genemic Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:22856251.

The sequence in this assembly is a combination of BAC based reads and Mhole genome shortgun sequencing reads assembled using Atlas and Mhole genome shortgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend departed the clone and there may be sequence Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A. D'Souza, L., Davila, M.L., Davis, C., Davis, C., Dederich, D., Deuglan, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Dragan-Rocha, S., Duni, A., Durbin, R., Durbin, R., Davis, C., Falls, T., contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature 2 (bases 1 to 217181)
Rat Genome Sequencing Consortium.
Direct Submission

us-10-085-612-2.rnpb

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August 27, 2003, 18:42:00; Search time 173.269 Seconds
. (without alignments)
450.193 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/U507_pUBCOMB.seq:*

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3: /cgn2_6/ptodata/2/pubpna,PCT_NR_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/U506_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna,NSO7_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna,NSO7_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna,NSO8_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna,NSO8_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna,NSO8_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna,NSO8_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna,NSO8_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna,NSO8_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna,NSO8_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna,NSO8_PUBCOMB.seq:*

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15: /cgn2_6/ptodata/2/pubpna,NSO8_PUBCOMB.seq:*

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19: /cgn2_6/ptodata/2/pubpna/USSO_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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34
1 cgattctttgctactggctgcagctgcagccccg 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1533700 seqs, 1147125425 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                             OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 14, Appl	Sequence 17, Appl	Sequence 72580, A	Sequence, 285947,	Sequence 41, Appl	Sequence 24594, A	Sequence 253693,	Sequence 489, App	Sequence 726, App
J.D.	US-10-085-612-2	US-10-085-612-6	US-10-085-612-4	US-09-957-997-4	US-10-146-575-3	US-10-085-612-3	US-09-957-997-1	US-10-121-960C-14	US-10-121-960C-17	US-10-027-632-72580	US-10-027-632-285947	US-10-215-432-41	US-09-918-995-24594	US-10-027-632-253693	US-09-934-455-489	US-09-770-149-726 S
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ייים הייי	34	34	1254	1012	1345	1345	11186	13035	15185	481	599	30	470	672	994	627
Match Length DB	100.0	97.1	97.1	67.1	67.1	67.1	67.1	67.1	67.1	63,5	62.9	9.09	59.4	59.4	59.4	58.8
Score	34	33	33	22.8	22.8	22.8	22.8	22.8	22.8	21.6	21.4	20.6	. 20.2	20.5	20.3	20
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RESULT 2 US-10-085-612-6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22.8; DB 10; Length 1012; Pred. No. 7; 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10146575
Publication No. US20030059800A1
GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Lichter, Jay
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: S2012P
CURRENT APPLICATION NUMBER: US/10/146,575
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE FEASTER 1998-08-31
SOFTWARE FEASTER FOR WINGOWS VERSION 3.0
SEQ ID NO 3
LENGTH: 1345
                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Berkenstam, Anders
APPLICANT: Berkenstam, Anders
APPLICANT: Berkenstam, Gran
APPLICANT: Berkenstam, Can
APPLICANT: Bromquist, Patrik
TILLE OF INVENTION: PROMOTER SEQUENCES
FILE REPRENCE: 13425-046001
CURRENT APPLICATION NUMBER: 05/09/957,997
CURRENT FILING DATE: 2001-09-21
EARLIER APPLICATION NUMBER: SE 0003393-6
EARLIER APPLICATION NUMBER: SE 0003393-6
EARLIER APPLICATION NUMBER: SE 0003393-6
EARLIER APPLICATION NUMBER: 06/238
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SOFTWARE FEACESQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1012
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Publication No. US20030096251A1
                                                        Sequence 4, Application US/09957997
Patent No. US20020150915A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.1%;
Best Local Similarity 92.3%;
Matches 24; Conservative C
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APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-997-4
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US-10-146-575-3
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                 US-09-957-997-4
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## APPLICANT: Vredenburgh, James

## APPLICANT: Vredenburgh, James

## APPLICANT: Vredenburgh, James

## APPLICANT: Orlvin, Ollver

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APPLICANT: Guida, Marco
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Petros, William
APPLICANT: Petros, William
APPLICANT: Petros, William
APPLICANT: Predemburgh, James
APPLICANT: Colvin, Oliver
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
TITLE OF INVENTION: Compositions Therefor
FILE REPERENCE: 4889-5-71
CURRENT APPLICATION NUMBER: 09/144,367
FRIOR FILING DATE: 2002-02-26
FRIOR FILING DATE: 2001-02-26
NUMBER: OF SOOL O2-26
NUMBER: OF SOOL O2-26
NUMBER: OF SOOL DATE: 2001-02-26
NUMBER: OF SOOL DATE: 2001-02-26
NUMBER: OF SOOL DATE: 2001-02-26
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0.00034;
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Pred. No. 0.00049;
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Sequence 6, Application US/10085612
Publication No. US20030096251A1
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10085612
Publication No. US20030096251A1
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SEQ ID NO 4
LENGTH: 1254
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US-10-085-612-4
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Best Local Similarity
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RESULT

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; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus US-10-121-960C-14
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APPLICANT: CONTAG, Pamela
APPLICANT: CONTAG, Pamela
APPLICANT: PURCHIO, Anthony
APPLICANT: HASHIMA, Sandy
APPLICANT: MA, Shirley
APPLICANT: MA, Shirley
TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF WITH
TITLE OF INVENTION: CYTOCHRONE EXPRESSION
TITLE OF INVENTION NUMBER: US/10/121,960C
CURRENT APPLICATION NUMBER: 2002-04-11
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH TITLE OF INVENTION: CTROCHROME PERPRESSION FILE REFERENCE: 9400-0014 / PAR-014.US CURRENT APPLICATION NUMBER: US/10/121,960C GURRENT PAILCATION NUMBER: US/10/121,960C WIRRENT FILING DATE: 2002-04-11 NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12860 TGCTACTGGCTGCAGCTCCAGCCCTG 12885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Matches 24; Conservative
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                                                                                                                                                                                                              SEQ ID NO 14
LENGTH: 13035
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US-10-121-960C-17
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             APPLICANT: Oldvin, Oliver
APPLICANT: Oldvin, Oliver
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
TITLE OF INVENTION: Compositions Therefor
FILE REPERENCE: 4389-5-C1
CURRENT FILING DATE: 2002-02-26
PRIOR PILING DATE: 2002-02-26
PRIOR PLICATION NUMBER: 09/144,367
PRIOR PLING DATE: 1998-08-31
PRIOR PLING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOUTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22.8; DB Pred. No. 7.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Berthenstam, Anders
APPLICANT: Berthenstam, Anders
APPLICANT: Berthenstam, Anders
APPLICANT: Berthenstam, Carn
APPLICANT: Bethenstam, Anders
TILE OF INVENTION: PROMOTER SEQUENCES
FILE REFRENCE: 1245-046001
CURRENT APPLICATION NUMBER: US/09/957, 997
CURRENT APPLICATION NUMBER: SE 0003393-6
EARLIER APPLICATION NUMBER: 60/238,895
EARLIER APPLICATION NUMBER: 60/238,895
BARLIER APPLICATION NUMBER: 60/238,895
NUMBER OF SEQ. ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
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; Patent No. US20020150915A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.1%;
Best Local Similarity 92.3%;
Matches 24; Conservative (
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APPLICANT: CONTAG, Pamela
APPLICANT: PUCKHIO, Anthony
APPLICANT: HASHINA, Sandy
APPLICANT: NA, Shirley
APPLICANT: NAWOYKA, Kevin
     Vredenburgh, James
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US-09-957-997-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-085-612-3
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Best Local Similarity
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LENGTH: 11186
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US-10-121-960C-14
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LENGTH: 1345
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Gaps
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                                                                     APPLICANT: Hetal Parekh-Olmedo
TITLE OF INYBATTON: Composition and methods for the
TITLE OF INVENTION: Composition and treatment of Huntington's disease
FILE REFERENCE: NaPro-10
CURRENT APPLICATION NUMBER: US/10/215,432
CURRENT PILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 44
SEQ ID NOS: 44
SEQ ID NO 41
LENGIH: 30
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Indentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827, 129
CURRENT EPPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
    APPLICANT: Hyeaq, Inc.
    TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
    TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
    FILE OF INVENTION: PROM VARIOUS cDNA LIBRARIES
    FILE REPERBAGNE: 20411-756
    CURRENT APPLICATION NUMBER: US/09/918,995
    PRIOR APPLICATION NUMBER: US/09/235,076
    PRIOR FILING DATE: 1999-01-20
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75.8%; Pred. No. 74;
tive 0; Mismatches
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SOFTWARE FastSEQ for Windows Version 3.0
SEQ ID NO 24594
LENGTH: 470
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; LCCATTON: (1)...(470)
; CTHER INFORMATION: n = A,T,C or G
US-09-918-995-24594
  US20030109476A1
                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Seguence
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Best Local Similarity 75.8'
Matches 25; Conservative
                                                APPLICANT: Eric B. Kmiec
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Publication No. US20
GENERAL INFORMATION:
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US-09-918-995-24594
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Sequence 285947, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPRENDENCE: 108827.129
CURRENT PILLING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILLING DATE: 2000-04-20
PRIOR FILLING DATE: 2000-03-29
PRIOR FILLING DATE: 2000-03-29
PRIOR FILLING DATE: 2000-03-29
PRIOR FILLING DATE: 2000-03-29
PRIOR FILLING DATE: 1999-11-23
PRIOR FILLING DATE: 1999-11-23
PRIOR FILLING DATE: 1999-11-23
PRIOR FILLING DATE: 1999-10-28
PRIOR FILLING DATE: 1999-10-28
PRIOR FILLING DATE: 1999-10-28
PRIOR FILLING DATE: 1999-10-28
PRIOR FILLING DATE: 1999-08-09
PRIOR FILLING DATE: 1999-08-09
PRIOR FILLING DATE: 1999-08-09
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                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR PELICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 72580
LENGTH: 481
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SOFTWARE: PastSEQ for Windows Version 4.0
                                                                     PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                    PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
  APPLICATION NUMBER: US 60/198,676
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US-10-215-432-41/c
; Sequence 41, Application US/10215432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%;
85.7%;
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Best Local Similarity 80.6:
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.73
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-10-027-632-285947/c
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                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Human
US-10-027-632-72580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 59.4%; Score 20.2; DB 13; Length 672; Best Local Similarity 75.8%; Pred. No. 77; Matches 25; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 489, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
APPLICANT: Adam, Luc.
APPLICANT: Adam, Luc.
APPLICANT: Dubell, Aroold
APPLICANT: Heard, Jacqueline
APPLICANT: Heard, Jacqueline
APPLICANT: Feddie, James
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Riechman, Jose Luis
APPLICANT: Richman, Jose Luis
APPLICANT: Richman, Jose Luis
APPLICANT: Pineda, Omaira
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT PILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOUTHARE: Patentin version 3.1
SEQ ID NO 489
TURNE: DATE
TURNE: DATE
TOWER DATE: 2010-04-17
SEQ ID NO 489
TURNE: DATE
TURNE: DATE: 2010-04-17
TERGIFF SEC ID NOS: 516
TURNER: PATENT PATENT DATE: 2010-04-17
TERGIFF SEC ID NOS: 516
TURNER: PATENT PATENT DATE: 2010-04-17
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,483
PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
SUPPLIED APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
SUPPLIED APPLICATION NUMBER: US 60/146,002
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; LOCATION: (1)..(711)
; OTHER INFORMATION: G2547
US-09-934-455-489
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US-10-027-632-253693
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Search completed: August 27, 2003, 21:14:09 Job time: 179.269 secs